



SUBSTITUTE SEQUENCE LISTING

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<120> CLASP-7 Transmembrane Protein

<130> 020054-000611US

<140> US 09/736,968

<141> 2000-12-13

<150> US 60/160,860

<151> 1999-10-21

<150> US 60/162,498

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<150> US 60/240,543

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<160> 115

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<170> PatentIn Ver. 2.1

<210> 1

<211> 6372

<212> DNA

<213> Homo sapiens

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<223> human CLASP-7

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Lys Leu Val Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile	
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Val Asn Leu Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser	
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Leu Val His Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys	
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Glu Pro Ser Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala	
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Thr Leu Ala Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg	
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Ser Lys Ser Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly	
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Ala Ile Leu Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser	
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Leu Arg Phe Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly	
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Cys Gly Ser Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu				
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1905								1910				1915				
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1920								1925				1930				
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1935								1940				1945				
gcc Ala	cag Gln	gtg Val	ttt Phe	tta Leu	gca Ala	gag Glu	atc Ile	ccg Pro	gaa Glu	gac Asp	ccc Pro	aag Lys	ctc Leu	ttc Phe	cgg Arg	5907
1950				1955				1960				1965				
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1985								1990				1995				
gag Glu	tac Tyr	cac His	cgt Arg	gag Glu	ctg Leu	gag Glu	cgc Arg	aac Asn	tac Tyr	tgc Cys	cgc Arg	ctg Leu	cgg Arg	gag Glu	gct Ala	6051
2000								2005				2010				
ctg Leu	cag Gln	ccc Pro	ctg Leu	ctt Leu	acc Thr	cag Gln	cgc Arg	ctg Leu	ccc Pro	cag Gln	ctg Leu	atg Met	gca Ala	ccc Pro	acc Thr	6099
2015				2020				2025								
cca Pro	ccc Pro	ggc Gly	ctc Leu	agg Arg	aac Asn	tcc Ser	ttg Leu	aac Asn	aga Arg	gca Ala	agt Ser	ttc Phe	cga Arg	aag Lys	gca Ala	6147
2030				2035				2040				2045				
gac ctc tga gcccacaagg accaaagctg tacctagagg aaccagcacc Asp Leu																6196
cgggcctcag ctgtctgtgc tgcgagggga gtctgccctg gtgccactg ggctgtgggg																6256
tgaccacact gtacttgggg ctgggccctc tgcccctgtg tccccatctg tgtgcactga																6316
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 Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
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 Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
 65 70 75 80
 Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
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 Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala
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 Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln
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 Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu
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 Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly
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 Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser
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 Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe
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 Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu
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 Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg
 210 215 220
 Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu
 225 230 235 240
 Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His
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 Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile
 260 265 270
 Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu
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 Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser
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 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr
 305 310 315 320
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 325 330 335

Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser
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 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys
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 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys
 370 375 380
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His
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 Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
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 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
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 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
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 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
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 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
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 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
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 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
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 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
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 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
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 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
 645 650 655
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe

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Cys	Leu	Pro	Val	Ser	Val	Asp	Gln	Pro	Pro	Pro	Ser	Tyr	Ser	Val	Leu		
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Thr	Pro	Asp	Val	Ala	Leu	Pro	Gly	Met	Arg	Trp	Val	Asp	Gly	His	Lys		
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Pro	Glu	Pro	Leu	Val	Ala	Phe	Ser	His	His	Val	Leu	Asp	Lys	Leu	Val		
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Gln	His	Ala	Trp	Phe	Phe	Phe	Gln	Leu	Met	Val	Lys	Ser	Met	Ala	Leu		
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 1570 1575 1580
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 1605 1610 1615
 Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala
 1620 1625 1630
 Leu Leu Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln

1635	1640	1645
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Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met 1685 1690 1695		
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Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly 1715 1720 1725		
Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp 1730 1735 1740		
Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His 1745 1750 1755 1760		
Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile 1765 1770 1775		
Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu 1780 1785 1790		
Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val 1795 1800 1805		
Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr 1810 1815 1820		
Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr 1825 1830 1835 1840		
Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe 1845 1850 1855		
Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg 1860 1865 1870		
Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg 1875 1880 1885		
Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val 1890 1895 1900		
Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr 1905 1910 1915 1920		
Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly 1925 1930 1935		
Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val 1940 1945 1950		
Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn 1955 1960 1965		

Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala
 1970 1975 1980

Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His
 1985 1990 1995 2000

Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro
 2005 2010 2015

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 2020 2025 2030

Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
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<211> 4

<212> PRT

<213> Artificial Sequence

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<210> 4

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP-7 homolog
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<400> 4

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<210> 5

<211> 10

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<222> (1)..(10)

<223> Xaa = any amino acid

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 Glu or Gln

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<210> 8

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 35 40 45
 Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys
 50 55 60
 Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn
 65 70 75 80
 Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His
 85 90 95
 Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys
 100 105 110
 Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu
 115 120 125

His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala
 130 135 140
 Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu
 145 150 155 160
 Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe
 165 170 175
 Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr
 180 185 190
 Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu
 195 200 205
 Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr
 210 215 220
 Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met
 225 230 235 240
 Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu
 245 250 255
 Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala
 260 265 270
 Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg
 275 280 285
 Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu
 290 295 300
 Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys
 305 310 315 320
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 325 330 335
 Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys
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 370 375 380
 Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu
 385 390 395 400
 Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly
 405 410 415
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 420 425 430
 Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser
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 Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala
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 Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu
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 Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser
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 Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr

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Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala
785					790					795					800
Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile
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Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe
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Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile
			835				840					845			
Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Glu	Thr
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Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp
865					870					875					880
Arg	Leu	Ile	Lys	His	Thr	Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	Leu	Thr
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Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys
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Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met
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Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Gly
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Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	Ala	Asp	Gly
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Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Phe	Glu	Asp	Glu	Asp
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Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His
1125 1130 1135

Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys
1140 1145 1150

Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
1155 1160 1165

Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr
1170 1175 1180

Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met
1185 1190 1195 1200

Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val
1205 1210 1215

Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln
1220 1225 1230

Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
1235 1240 1245

Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
1250 1255 1260

Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
1265 1270 1275 1280

Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
1285 1290 1295

Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
1300 1305 1310

Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
1315 1320 1325

Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
1330 1335 1340

Met Thr Ser Ser Ser Ser Val Val
1345 1350

<210> 10

<211> 1534

<212> PRT

<213> Homo sapiens

<220>

<223> human KIAA1058

<400> 10

Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
1 5 10 15

Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
 20 25 30
 Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
 35 40 45
 Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
 50 55 60
 Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
 65 70 75 80
 Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
 85 90 95
 His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
 100 105 110
 Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
 115 120 125
 Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
 130 135 140
 Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
 145 150 155 160
 Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
 165 170 175
 Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
 180 185 190
 Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
 195 200 205
 Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
 210 215 220
 Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
 225 230 235 240
 Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
 245 250 255
 Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly
 260 265 270
 Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
 275 280 285
 Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
 290 295 300
 Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
 305 310 315 320
 Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
 325 330 335

Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
 340 345 350
 Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
 355 360 365
 Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
 370 375 380
 Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
 385 390 395 400
 Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu
 405 410 415
 Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Asp Val Leu
 420 425 430
 Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu
 435 440 445
 Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
 450 455 460
 Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
 465 470 475 480
 Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
 485 490 495
 Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
 500 505 510
 Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu
 515 520 525
 Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile
 530 535 540
 Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr
 545 550 555 560
 Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn
 565 570 575
 His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
 580 585 590
 Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
 595 600 605
 Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln
 610 615 620
 Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu
 625 630 635 640
 Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn
 645 650 655
 Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn

660					665					670					
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His
	675						680					685			
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr
	690					695					700				
Ser	Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser
705					710					715					720
Leu	Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu
				725					730					735	
Lys	Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn
			740					745					750		
Ser	Val	Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu
	755					760						765			
Leu	Met	Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu
	770				775						780				
Phe	Thr	Tyr	Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe
785				790						795					800
Thr	Ile	Ser	Glu	Val	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg
				805					810					815	
Tyr	Ile	Ala	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	Leu	Gly
			820					825					830		
Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	Ser	Asp
		835					840					845			
Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	Thr	Glu
	850					855					860				
Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu	Ala	Phe
865				870						875				880	
Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met	Lys	Lys
			885					890					895		
Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser	Glu	Thr
		900						905					910		
Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr	Lys	Phe
	915						920					925			
Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala	Leu	Cys
	930					935					940				
Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile	Arg	Thr
945				950						955				960	
Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe	Asp	Tyr
			965						970					975	
Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile	Ile	Ser
			980					985					990		

Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
 995 1000 1005
 Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
 1010 1015 1020
 Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
 1025 1030 1035 1040
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
 1045 1050 1055
 Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
 1060 1065 1070
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
 1075 1080 1085
 Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
 1090 1095 1100
 His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
 1105 1110 1115 1120
 Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
 1125 1130 1135
 Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
 1140 1145 1150
 Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
 1155 1160 1165
 Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
 1170 1175 1180
 Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
 1185 1190 1195 1200
 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
 1205 1210 1215
 Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
 1220 1225 1230
 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
 1235 1240 1245
 Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
 1250 1255 1260
 Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 1265 1270 1275 1280
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 1285 1290 1295
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 1300 1305 1310

Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
 1315 1320 1325

Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 1330 1335 1340

Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
 1345 1350 1355 1360

Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 1365 1370 1375

Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 1380 1385 1390

Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 1395 1400 1405

Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 1410 1415 1420

Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 1425 1430 1435 1440

Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 1445 1450 1455

Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 1460 1465 1470

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 1475 1480 1485

Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 1490 1495 1500

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 1505 1510 1515 1520

Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
 1525 1530

<210> 11

<211> 738

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat TRG

<400> 11

Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val
 1 5 10 15

Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
 20 25 30

Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
 35 40 45

Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
 50 55 60
 Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
 65 70 75 80
 Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
 85 90 95
 Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
 100 105 110
 Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
 115 120 125
 Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr
 130 135 140
 Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val
 145 150 155 160
 Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met
 165 170 175
 Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro
 180 185 190
 Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys
 195 200 205
 Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala
 210 215 220
 Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Asp Leu Ala Leu Gln
 225 230 235 240
 Arg Glu Pro Pro Val Phe Pro Tyr Ser His Thr Ser Cys Gln Arg Lys
 245 250 255
 Ser Arg Gly Gly Met Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 260 265 270
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 275 280 285
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 290 295 300
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Leu Arg Ala Gly Leu Leu
 305 310 315 320
 Thr Ser Ile Asn Ser Ser Ser Pro Ser Met Lys Ser Gly Gly Thr Leu
 325 330 335
 Glu Thr Thr His Leu Tyr Asp Thr Leu His Arg Pro Tyr Ser Lys Val
 340 345 350
 Thr Glu Val Ile Thr Arg Ala Ala Gly Ser Trp Asp Leu Leu Pro Gly
 355 360 365
 Gly Leu Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr

370	375	380
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg		
385	390	395 400
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met		
	405	410 415
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe		
	420	425 430
Ala Tyr Ile Gln Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu		
	435	440 445
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Cys His Asn Ile Arg Arg		
	450	455 460
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly		
465	470	475 480
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys		
	485	490 495
Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr		
	500	505 510
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val		
	515	520 525
Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys		
	530	535 540
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly		
545	550	555 560
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg		
	565	570 575
Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe		
	580	585 590
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys		
	595	600 605
Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu		
	610	615 620
Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly		
625	630	635 640
Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln		
	645	650 655
Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu		
	660	665 670
Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val		
	675	680 685
Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln		
	690	695 700

Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr
705 710 715 720

Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile
725 730 735

Phe Phe

<210> 12

<211> 1214

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-4

<400> 12

Met Glu Ile Gln Val Leu Ile Arg Phe Leu Ser Val Ile Leu Met Gln
1 5 10 15

Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
20 25 30

Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
35 40 45

Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
50 55 60

Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
65 70 75 80

Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
85 90 95

Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys
100 105 110

Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
115 120 125

Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
130 135 140

Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
145 150 155 160

Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
165 170 175

Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
180 185 190

Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
195 200 205

Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
210 215 220

Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser
 225 230 235 240
 Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu
 245 250 255
 Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr
 260 265 270
 Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys
 275 280 285
 His Ala Phe Asp Thr Arg Tyr Gln His Lys Asn Gln Gln Ala Lys Ile
 290 295 300
 Ala Gln Leu Tyr Leu Pro Phe Val Gly Leu Leu Leu Glu Asn Ile Gln
 305 310 315 320
 Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn
 325 330 335
 Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn
 340 345 350
 Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln
 355 360 365
 Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro
 370 375 380
 Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr
 385 390 395 400
 Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp
 405 410 415
 Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys
 420 425 430
 Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro
 435 440 445
 Gln Glu Leu Ile Asn Ile Leu Ile Leu Leu Glu Val Cys Leu Phe His
 450 455 460
 Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp
 465 470 475 480
 Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala
 485 490 495
 Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser
 500 505 510
 Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu
 515 520 525
 Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu
 530 535 540
 Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe

545		550		555		560
Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys						
	565			570		575
Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val						
	580		585		590	
Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe						
	595	600		605		
Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys						
	610	615		620		
Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn						
625		630		635		640
Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr						
	645		650		655	
Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala						
	660		665		670	
Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe						
	675		680		685	
Gln Glu Ser Leu Phe Ile Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro						
690		695		700		
Met Leu Ala Arg Ala Phe Pro Ala Glu Val Lys Asp Leu Thr Lys Arg						
705		710		715		720
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Lys						
	725		730		735	
Asp Pro Glu Met Leu Ile Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr						
	740		745		750	
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Lys						
	755		760		765	
Ile His Val Lys Asn Gly Asp Phe Ser Glu Ala Ala Met Cys Tyr Val						
	770		775		780	
His Val Ala Ala Leu Val Ala Glu Phe Leu His Arg Lys Lys Leu Phe						
785		790		795		800
Pro Asn Gly Cys Ser Ala Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu						
	805		810		815	
Glu Gly Ala Met Lys Glu Asp Ala Gly Met Met Asp Val His Tyr Ser						
	820		825		830	
Glu Glu Val Leu Leu Glu Leu Leu Glu Gln Cys Val Asn Gly Leu Trp						
	835		840		845	
Lys Ala Glu Arg Tyr Glu Ile Ile Ser Glu Ile Ser Lys Leu Ile Gly						
	850		855		860	
Pro Ile Tyr Glu Asn Arg Arg Glu Phe Glu Asn Leu Thr Gln Val Tyr						
865		870		875		880

Arg Thr Leu His Gly Ala Tyr Thr Lys Ile Leu Glu Val Met His Thr
 885 890 895
 Lys Lys Arg Leu Leu Gly Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln
 900 905 910
 Ser Phe Phe Glu Glu Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 915 920 925
 Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr
 930 935 940
 Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser Asp
 945 950 955 960
 Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val
 965 970 975
 Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys
 980 985 990
 Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala
 995 1000 1005
 Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
 1010 1015 1020
 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
 1025 1030 1035 1040
 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
 1045 1050 1055
 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
 1060 1065 1070
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
 1075 1080 1085
 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
 1090 1095 1100
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
 1105 1110 1115 1120
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
 1125 1130 1135
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
 1140 1145 1150
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
 1155 1160 1165
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
 1170 1175 1180
 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
 1185 1190 1195 1200

Met 1	Ser	Phe	Leu	Pro 5	Ile	Ile	Leu	Asn	Gln	Leu	Phe	Lys	Val	Leu	Val 15
Gln	Asn	Glu	Glu	Asp 20	Glu	Ile	Thr	Thr 25	Thr	Val	Thr	Arg	Val 30	Leu	Pro
Asp	Ile	Val 35	Ala	Lys	Cys	His	Glu 40	Glu	Gln	Leu	Asp	His 45	Ser	Val	Gln
Ser	Tyr 50	Ile	Lys	Phe	Val	Phe 55	Lys	Thr	Arg	Ala	Cys 60	Lys	Glu	Arg	Pro
Val 65	His	Glu	Asp	Leu	Ala 70	Lys	Asn	Val	Thr	Gly 75	Leu	Leu	Lys	Ser	Asn 80
Asp	Ser	Pro	Thr	Val 85	Lys	His	Val	Leu	Lys 90	His	Ser	Trp	Phe	Phe 95	Phe
Ala	Ile	Ile	Leu 100	Lys	Ser	Met	Ala	Gln 105	His	Leu	Ile	Asp	Thr 110	Asn	Lys
Ile	Gln 115	Leu	Pro	Arg	Pro	Gln 120	Arg	Phe	Pro	Glu	Ser	Tyr 125	Gln	Asn	Glu
Leu 130	Asp	Asn	Leu	Val	Met	Val 135	Leu	Ser	Asp	His	Val 140	Ile	Trp	Lys	Tyr
Lys 145	Asp	Ala	Leu	Glu	Glu 150	Thr	Arg	Arg	Ala	Thr 155	His	Ser	Val	Ala	Arg 160
Phe	Leu	Lys	Arg	Cys 165	Phe	Thr	Phe	Met	Asp 170	Arg	Gly	Cys	Val	Phe 175	Lys
Met	Val	Asn 180	Asn	Tyr	Ile	Ser	Met	Phe 185	Ser	Ser	Gly	Asp	Leu 190	Lys	Thr
Leu	Cys 195	Gln	Tyr	Lys	Phe	Asp	Phe 200	Leu	Gln	Glu	Val	Cys 205	Gln	His	Glu
His 210	Phe	Ile	Pro	Leu	Cys	Leu 215	Pro	Ile	Arg	Ser	Ala 220	Asn	Ile	Pro	Asp
Pro 225	Leu	Thr	Pro	Ser	Glu 230	Ser	Thr	Gln	Glu	Leu 235	His	Ala	Ser	Asp	Met 240
Pro	Glu	Tyr	Ser	Val 245	Thr	Asn	Glu	Phe	Cys 250	Arg	Lys	His	Phe	Leu 255	Ile

Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp
 260 265 270
 Val Arg His Leu Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His
 275 280 285
 Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala
 290 295 300
 Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg
 305 310 315 320
 Ile Tyr Leu Lys Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln
 325 330 335
 Gly Ser Arg Asp Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr
 340 345 350
 Ala Ile Lys His Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val
 355 360 365
 Leu Asn Ser Ile Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn
 370 375 380
 His Ala Asp Ser Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser
 385 390 395 400
 Thr Asn Glu Lys Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro
 405 410 415
 Arg Pro Leu Ala Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp
 420 425 430
 Gln Ala Glu Thr Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys
 435 440 445
 Thr Ile Ser Tyr Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser
 450 455 460
 Pro Glu Val Ser Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn
 465 470 475 480
 Phe Arg Tyr Leu Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala
 485 490 495
 Phe Lys Phe Val Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser
 500 505 510
 Asn Pro Ser Cys Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser
 515 520 525
 Thr Ser Arg His Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro
 530 535 540
 Ile Ile Arg Gly Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met
 545 550 555 560
 Leu Asp Asn Thr Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His
 565 570 575
 His Val Asp Thr Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile

580					585					590					
Leu	Asp	Leu	Val	Ser	Leu	Phe	Thr	Gln	Thr	His	Gln	Arg	Gln	Leu	Gln
	595						600					605			
Gln	Cys	Asp	Cys	Gln	Asn	Ser	Leu	Met	Lys	Arg	Gly	Phe	Asp	Thr	Tyr
	610					615					620				
Met	Leu	Phe	Phe	Gln	Val	Asn	Gln	Ser	Ala	Thr	Ala	Leu	Lys	His	Val
	625					630					635				640
Phe	Ala	Ser	Leu	Arg	Leu	Phe	Val	Cys	Lys	Phe	Pro	Ser	Ala	Phe	Phe
				645					650					655	
Gln	Gly	Pro	Ala	Asp	Leu	Cys	Gly	Ser	Phe	Cys	Tyr	Glu	Val	Leu	Lys
			660					665					670		
Cys	Cys	Asn	His	Arg	Ser	Arg	Ser	Thr	Gln	Thr	Glu	Ala	Ser	Ala	Leu
		675					680					685			
Leu	Tyr	Leu	Phe	Met	Arg	Lys	Asn	Phe	Glu	Phe	Asn	Lys	Gln	Lys	Ser
	690					695					700				
Ile	Val	Arg	Ser	His	Leu	Gln	Leu	Ile	Lys	Ala	Val	Ser	Gln	Leu	Ile
	705					710					715				720
Ala	Asp	Ala	Gly	Ile	Gly	Gly	Ser	Arg	Phe	Gln	His	Ser	Leu	Ala	Ile
				725					730					735	
Thr	Asn	Asn	Phe	Ala	Asn	Gly	Asp	Lys	Gln	Met	Lys	Asn	Ser	Asn	Phe
			740					745					750		
Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met
		755					760					765			
Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	Asp	Pro	Glu	Met	Leu	Val
	770					775					780				
Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Asn	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu
	785					790					795				800
Arg	Arg	Thr	Trp	Leu	Glu	Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly
				805					810					815	
Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Ile	His	Ile	Ala	Ala	Leu	Ile
			820					825					830		
Ala	Glu	Tyr	Leu	Lys	Arg	Lys	Gly	Tyr	Trp	Lys	Val	Glu	Lys	Ile	Cys
		835					840					845			
Thr	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Thr	His	Pro	Cys	Asp	Ser	Asn	Ser
	850						855					860			
Leu	Leu	Thr	Thr	Pro	Ser	Gly	Gly	Ser	Met	Phe	Ser	Met	Gly	Trp	Pro
	865					870					875				880
Ala	Phe	Leu	Ser	Ile	Thr	Pro	Asn	Ile	Lys	Glu	Glu	Gly	Ala	Ala	Lys
				885					890					895	
Glu	Asp	Ser	Gly	Met	His	Asp	Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val
			900					905					910		

Glu Gln Leu Tyr Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr
 915 920 925
 Glu Leu Ile Ala Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys
 930 935 940
 Gln Arg Asp Phe Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg
 945 950 955 960
 Ser Tyr Leu Lys Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe
 965 970 975
 Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu
 980 985 990
 Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu
 995 1000 1005
 Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly
 1010 1015 1020
 Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
 1025 1030 1035 1040
 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
 1045 1050 1055
 Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
 1060 1065 1070
 His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
 1075 1080 1085
 Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
 1090 1095 1100
 Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
 1105 1110 1115 1120
 Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
 1125 1130 1135
 Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
 1140 1145 1150
 Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
 1155 1160 1165
 Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
 1170 1175 1180
 Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
 1185 1190 1195 1200
 Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
 1205 1210 1215
 Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
 1220 1225 1230

Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn
 1235 1240 1245

Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
 1250 1255 1260

Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
 1265 1270 1275 1280

Ser Ile Ser Ser Ser Ala Glu Val
 1285

<210> 14

<211> 1220

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-3

<400> 14

Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn
 1 5 10 15

Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp
 20 25 30

Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile
 35 40 45

Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly
 50 55 60

Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser
 65 70 75 80

Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu
 85 90 95

Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys
 100 105 110

Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser
 115 120 125

Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met
 130 135 140

Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala
 145 150 155 160

Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala
 165 170 175

Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp
 180 185 190

Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn
 195 200 205

Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys
 210 215 220
 Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro
 225 230 235 240
 Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser
 245 250 255
 His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro
 260 265 270
 Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser
 275 280 285
 Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu
 290 295 300
 Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu
 305 310 315 320
 Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly
 325 330 335
 Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His
 340 345 350
 Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala
 355 360 365
 Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln
 370 375 380
 Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys
 385 390 395 400
 Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln
 405 410 415
 Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg
 420 425 430
 Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr
 435 440 445
 Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val
 450 455 460
 Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu
 465 470 475 480
 Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val
 485 490 495
 Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser
 500 505 510
 Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala
 515 520 525
 Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg

530	535	540
Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu 545 550 555 560		
Asn Leu Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu 565 570 575		
Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp 580 585 590		
Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu 595 600 605		
Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu 610 615 620		
Gly Gly Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser 625 630 635 640		
Ala Val Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser 645 650 655		
Lys Phe Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp 660 665 670		
Leu Cys Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile 675 680 685		
Arg Ser His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe 690 695 700		
Glu Ile Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser 705 710 715 720		
Leu Ser Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu 725 730 735		
Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu 740 745 750		
Leu Arg Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn 755 760 765		
Leu His Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu 770 775 780		
Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr 785 790 795 800		
Gln Thr Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly 805 810 815		
Lys His Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val 820 825 830		
His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg 835 840 845		
Lys Tyr Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn 850 855 860		

Val	Leu	Glu	Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	865				870					875					880	
Glu	Gly	Ile	Cys	Ser	Gly	Lys	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly		885						890						895		
Leu	Leu	Glu	Gln	Ala	Ala	Ala	Ser	Phe	Ser	Met	Ala	Gly	Met	Tyr	Glu			900					905					910			
Ala	Val	Asn	Glu	Val	Tyr	Lys	Val	Leu	Ile	Pro	Ile	His	Glu	Ala	Asn		915						920					925			
Arg	Asp	Ala	Lys	Lys	Leu	Ser	Thr	Ile	His	Gly	Lys	Leu	Gln	Glu	Ala		930						935					940			
Phe	Ser	Lys	Ile	Val	His	Gln	Ser	Thr	Gly	Trp	Glu	Arg	Met	Phe	Gly		945						950					955		960	
Thr	Tyr	Phe	Arg	Val	Gly	Phe	Tyr	Gly	Thr	Lys	Phe	Gly	Asp	Leu	Asp			965							970				975		
Glu	Gln	Glu	Phe	Val	Tyr	Lys	Glu	Pro	Ala	Ile	Thr	Lys	Leu	Ala	Glu				980						985				990		
Ile	Ser	His	Arg	Leu	Glu	Gly	Phe	Tyr	Gly	Glu	Arg	Phe	Gly	Glu	Asp				995						1000				1005		
Val	Val	Glu	Val	Ile	Lys	Asp	Ser	Asn	Pro	Val	Asp	Lys	Cys	Lys	Leu		1010								1015				1020		
Asp	Pro	Asn	Lys	Ala	Tyr	Ile	Gln	Ile	Thr	Tyr	Val	Glu	Pro	Tyr	Phe		1025								1030				1035		1040
Asp	Thr	Tyr	Glu	Met	Lys	Asp	Arg	Ile	Thr	Tyr	Phe	Asp	Lys	Asn	Tyr				1045						1050				1055		
Asn	Leu	Arg	Arg	Phe	Met	Tyr	Cys	Thr	Pro	Phe	Thr	Leu	Asp	Gly	Arg				1060						1065				1070		
Ala	His	Gly	Glu	Leu	His	Glu	Gln	Phe	Lys	Arg	Lys	Thr	Ile	Leu	Thr				1075						1080				1085		
Thr	Ser	His	Ala	Phe	Pro	Tyr	Ile	Lys	Thr	Arg	Val	Asn	Val	Thr	His		1090								1095				1100		
Lys	Glu	Glu	Ile	Ile	Leu	Thr	Pro	Ile	Glu	Val	Ala	Ile	Glu	Asp	Met				1105						1110				1115		1120
Gln	Lys	Lys	Thr	Gln	Glu	Leu	Ala	Phe	Ala	Thr	His	Gln	Asp	Pro	Ala					1125						1130				1135	
Asp	Pro	Lys	Met	Leu	Gln	Met	Val	Leu	Gln	Gly	Ser	Val	Gly	Thr	Thr				1140							1145				1150	
Val	Asn	Gln	Gly	Pro	Leu	Glu	Val	Ala	Gln	Val	Phe	Leu	Ser	Glu	Ile				1155							1160				1165	
Pro	Ser	Asp	Pro	Lys	Leu	Phe	Arg	His	His	Asn	Lys	Leu	Arg	Leu	Cys		1170									1175				1180	

Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys
 1185 1190 1195 1200

Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys
 1205 1210 1215

Leu Ser Ser Pro
 1220

<210> 15

<211> 987

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-5

<400> 15

Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser
 1 5 10 15

Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser
 20 25 30

Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro
 35 40 45

Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu
 50 55 60

Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu
 65 70 75 80

Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys
 85 90 95

Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp
 100 105 110

Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr
 115 120 125

Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr
 130 135 140

Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr
 145 150 155 160

Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu
 165 170 175

Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met
 180 185 190

Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro
 195 200 205

Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu
 210 215 220

Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln
 225 230 235 240
 Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu Ala Leu
 245 250 255
 Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg Ala Pro
 260 265 270
 Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp Lys Lys
 275 280 285
 Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys Thr Lys
 290 295 300
 Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala Thr Glu
 305 310 315 320
 Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln Ala Ser
 325 330 335
 Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly Val Leu Arg Val
 340 345 350
 Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr Tyr Leu Thr His
 355 360 365
 Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp Leu Leu
 370 375 380
 Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln Val Leu
 385 390 395 400
 His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala Cys Ala
 405 410 415
 Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser Asn Phe
 420 425 430
 Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu Val Gly
 435 440 445
 Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu Arg Thr
 450 455 460
 Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr Pro Phe
 465 470 475 480
 Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile Leu Tyr
 485 490 495
 Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met Leu Met
 500 505 510
 Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro Asp Leu
 515 520 525
 Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys Lys Lys
 530 535 540
 Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala Leu Val

545		550		555		560
Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly						
	565		570		575	
Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val						
	580		585		590	
Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly						
	595		600		605	
Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala						
	610		615		620	
Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr						
	625		630		635	640
Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu						
	645		650		655	
Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn						
	660		665		670	
Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe						
	675		680		685	
Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu						
	690		695		700	
Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe						
	705		710		715	720
Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser						
	725		730		735	
Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln						
	740		745		750	
Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg						
	755		760		765	
Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr						
	770		775		780	
Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln						
	785		790		795	800
Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile						
	805		810		815	
Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro						
	820		825		830	
Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala						
	835		840		845	
Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val						
	850		855		860	
Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val						
	865		870		875	880

Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg
 885 890 895

His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
 900 905 910

Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
 915 920 925

Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
 930 935 940

Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
 945 950 955 960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
 965 970 975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
 980 985

<210> 16

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-1

<400> 16

Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
 1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

<210> 17

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
 and B from human KIAA1058

<400> 17

Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp
 1 5 10 15

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
 20 25 30

Tyr Ile Tyr Lys Glu Pro
 35

<210> 18

<211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif B
 from human CLASP-2

<400> 18
 Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 1 5 10

<210> 19
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-6

<400> 19
 Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
 1 5 10 15
 Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

<210> 20
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-4

<400> 20
 Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
 1 5 10 15
 Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

<210> 21
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from canonical DOCK180

<400> 21
 Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
 1 5 10 15
 Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp

20

25

30

<210> 22

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK2

<400> 22

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
1 5 10 15Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 23

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK3

<400> 23

Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15Lys Glu Tyr Val Cys Arg Gly His
20

<210> 24

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA0716

<400> 24

Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15Lys Glu Phe Val Cys Arg Gly His
20

<210> 25

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A

and B from human CLASP-3

<400> 25

Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro
20

<210> 26

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from rat TRG

<400> 26

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
35 40 45

Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 27

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-1

<400> 27

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
20 25 30

Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
35 40 45

Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
50 55 60

<210> 28

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-2

<400> 28

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
20 25 30Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
35 40 45Val Thr His Val Ile Pro Phe Asp Glu Lys Glu
50 55 60

<210> 29

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-4

<400> 29

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
1 5 10 15Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
20 25 30Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
35 40 45Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
50 55 60

<210> 30

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-3

<400> 30

Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
1 5 10 15Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
20 25 30Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
35 40 45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu

50

55

60

<210> 31
 <211> 54
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human KIAA0716

<400> 31
 His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
 1 5 10 15
 Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
 20 25 30
 Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
 35 40 45
 Ile Pro Glu Ser Gln Glu
 50

<210> 32
 <211> 54
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from canonical DOCK3

<400> 32
 His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
 1 5 10 15
 Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
 20 25 30
 Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
 35 40 45
 Ile Pro Asp Tyr Val Asp
 50

<210> 33
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from canonical DOCK2

<400> 33
 Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
 1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
 20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
 35 40 45

<210> 34

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
 from canonical DOCK180

<400> 34

Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
 1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
 20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
 35 40 45

Leu Asp Glu His Pro
 50

<210> 35

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-1

<400> 35

Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
 35 40 45

<210> 36

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
 and E from rat TRG

<400> 36

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
 35 40 45

<210> 37

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
 and E from human KIAA1058

<400> 37

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40 45

<210> 38

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-2

<400> 38

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40 45

<210> 39

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-6

<400> 39

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg

1 5 10 15
 Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40

<210> 40
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-4

<400> 40
 Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
 20 25 30

Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
 35 40 45

<210> 41
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-3

<400> 41
 Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
 1 5 10 15

Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
 20 25 30

Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
 35 40 45

<210> 42
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-5

<400> 42
 Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
 1 5 10 15

Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
35 40 45

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<210> 43
<211> 45
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human KIAA0716

<400> 43
Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
1 5 10 15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
20 25 30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
35 40 45

```
<210> 44
<211> 45
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from canonical DOCK2
```

<400> 44
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
35 40 45

```
<210> 45
<211> 45
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from canonical DOCK3
```

<400> 45
Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
1 5 10 15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn
 20 25 30

Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
 35 40 45

<210> 46

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK180

<400> 46

Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 47

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-1

<400> 47

Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
 1 5 10 15

Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
 20 25 30

Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
 35 40 45

Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
 50 55

<210> 48

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
 and G from rat TRG

<400> 48

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala

1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30
 Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45
 Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
 50 55

<210> 49
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human KIAA1058

<400> 49
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30
 Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45
 Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
 50 55

<210> 50
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-2

<400> 50
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30
 Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45
 Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
 50 55

<210> 51
 <211> 58
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-6

<400> 51

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 52

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-3

<400> 52

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
50 55

<210> 53

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-4

<400> 53

Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
35 40 45

Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
50 55

<210> 54
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-5

<400> 54
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
20 25 30

Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
35 40 45

Phe Ile Met Arg Cys Gly Glu Ala Val Glu
50 55

<210> 55
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA0716

<400> 55
Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
1 5 10 15

Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
20 25 30

Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
35 40 45

Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
50 55 60

<210> 56
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from canonical DOCK2

<400> 56

```

Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1               5               10               15
Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
                20               25               30
Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
                35               40               45
Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
                50               55               60

```

```

<210> 57
<211> 60
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:DOCK motifs F
      and G from canonical DOCK3

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```

<400> 57
Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1               5               10               15
Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
                20               25               30
Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
                35               40               45
Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
                50               55               60

```

```

<210> 58
<211> 60
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence:DOCK motifs F
      and G from canonical DOCK180

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```

<400> 58
Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1               5               10               15
Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
                20               25               30
Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
                35               40               45
Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg
                50               55               60

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<210> 59
<211> 2149

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<212> DNA
 <213> Homo sapiens

<220>
 <223> preliminary human CLASP-7 cDNA sequence

<220>
 <221> CDS
 <222> (2) .. (1933)
 <223> human CLASP-7

<400> 59

c ctt tca gaa gcc cgg gag agc gtc ttg ggg gat ttg ctg aag gtt gtg 49
 Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Asp Leu Leu Lys Val Val
 1 5 10 15

ctg tac agc ctg ggc agt gcc cag agt gcc ctc ttc ttg cag cat ggc 97
 Leu Tyr Ser Leu Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly
 20 25 30

ctg gcc acc cag agg gcc ctt gtg tcc aag ttc ccg gag ctg ctg ttc 145
 Leu Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe
 35 40 45

gag gag gac acg gag ctg tgt gcc gac ctg tgc ctg agg ctc cta cga 193
 Glu Glu Asp Thr Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg
 50 55 60

cac tgt ggc agc cgc atc agc acc atc cgc acg cac gcc agc gcc tcg 241
 His Cys Gly Ser Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser
 65 70 75 80

ctg tac ctg ctc atg cga cag aac ttc gag atc gcc cac aac ttt gcc 289
 Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala
 85 90 95

cgt gtg aag atg cag gtc acc atg tct ctc tcg tcc ctg gtg ggg acg 337
 Arg Val Lys Met Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr
 100 105 110

acg cag aac ttc agt gaa gag cac ctg cga cgt tca ctc aaa acc atc 385
 Thr Gln Asn Phe Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile
 115 120 125

ctc acc tat gct gag gag gac atg ggg ctg cgg gac agc acc ttc gca 433
 Leu Thr Tyr Ala Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala
 130 135 140

gag cag gtc cag gac ctg atg ttc aac ctg cac atg atc ctg acg gac 481
 Glu Gln Val Gln Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp
 145 150 155 160

acg gtg aag atg aag gaa cac cag gag gac cct gag atg ctc atc gac 529
 Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp
 165 170 175

ctc atg tac aga att gcc cgg ggc tac cag ggc tca ccg gac ctt cgg 577
 Leu Met Tyr Arg Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg
 180 185 190

ctg acc tgg ttg cag aac atg gcc ggg aag cac gcg gag ctg ggc aac 625

Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	Lys	His	Ala	Glu	Leu	Gly	Asn	
		195					200					205				
cac	gcc	gag	gcc	gcc	cag	tgc	atg	gtg	cac	gcg	gcc	gcc	ctc	gtg	gct	673
His	Ala	Glu	Ala	Ala	Gln	Cys	Met	Val	His	Ala	Ala	Ala	Leu	Val	Ala	
	210					215					220					
gag	tac	ctc	gcc	ctg	ctc	gag	gac	cac	cgc	cac	ctg	ccc	gtg	ggc	tgc	721
Glu	Tyr	Leu	Ala	Leu	Leu	Glu	Asp	His	Arg	His	Leu	Pro	Val	Gly	Cys	
225					230					235					240	
gtt	tcc	ttc	cag	aac	atc	tca	tcc	aat	gtg	cta	gag	gag	tcc	gcc	atc	769
Val	Ser	Phe	Gln	Asn	Ile	Ser	Ser	Asn	Val	Leu	Glu	Glu	Ser	Ala	Ile	
				245					250					255		
tcc	gac	gac	atc	ctg	tcg	ccc	gac	gag	gag	ggc	ttc	tgc	tcc	ggg	aag	817
Ser	Asp	Asp	Ile	Leu	Ser	Pro	Asp	Glu	Glu	Gly	Phe	Cys	Ser	Gly	Lys	
			260					265					270			
cac	ttc	act	gag	ctg	ggg	ctg	gta	ggg	ttg	ctg	gaa	cag	gca	gcc	ggc	865
His	Phe	Thr	Glu	Leu	Gly	Leu	Val	Gly	Leu	Leu	Glu	Gln	Ala	Ala	Gly	
		275					280					285				
tac	ttc	acc	atg	ggc	ggg	ctc	tac	gag	gcg	gtg	aat	gag	gtc	tac	aag	913
Tyr	Phe	Thr	Met	Gly	Gly	Leu	Tyr	Glu	Ala	Val	Asn	Glu	Val	Tyr	Lys	
	290					295					300					
aac	ctc	atc	ccc	atc	ctg	gaa	gcc	cac	cgt	gac	tac	aag	aag	ctg	gcc	961
Asn	Leu	Ile	Pro	Ile	Leu	Glu	Ala	His	Arg	Asp	Tyr	Lys	Lys	Leu	Ala	
305					310					315					320	
gcg	gtg	cac	ggc	aaa	ctg	cag	gag	gcc	ttc	acc	aag	atc	atg	cac	cag	1009
Ala	Val	His	Gly	Lys	Leu	Gln	Glu	Ala	Phe	Thr	Lys	Ile	Met	His	Gln	
				325					330					335		
agt	tcc	ggc	tgg	gag	cgc	gtg	ttc	ggg	acg	tat	ttc	cgc	gtg	ggc	ttc	1057
Ser	Ser	Gly	Trp	Glu	Arg	Val	Phe	Gly	Thr	Tyr	Phe	Arg	Val	Gly	Phe	
			340					345					350			
tac	ggc	gcc	cac	ttc	ggt	gac	ctg	gat	gag	cag	gag	ttt	gtg	tac	aag	1105
Tyr	Gly	Ala	His	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	Lys	
		355				360						365				
gag	cca	tcg	atc	acg	aag	ctg	gca	gag	atc	tca	cac	cgg	ctg	gag	gag	1153
Glu	Pro	Ser	Ile	Thr	Lys	Leu	Ala	Glu	Ile	Ser	His	Arg	Leu	Glu	Glu	
	370					375					380					
ttc	tac	acg	gag	aga	ttt	ggc	gac	gac	gtc	gtt	gag	att	atc	aaa	gac	1201
Phe	Tyr	Thr	Glu	Arg	Phe	Gly	Asp	Asp	Val	Val	Glu	Ile	Ile	Lys	Asp	
385					390					395				400		
tct	tac	cct	gtg	gac	aag	tcc	aag	ctt	gac	tca	caa	aag	gcc	tac	atc	1249
Ser	Tyr	Pro	Val	Asp	Lys	Ser	Lys	Leu	Asp	Ser	Gln	Lys	Ala	Tyr	Ile	
				405				410					415			
cag	atc	acg	tat	gtg	gaa	cgc	tac	ttt	gat	acc	tac	gag	ctc	aag	gac	1297
Gln	Ile	Thr	Tyr	Val	Glu	Pro	Tyr	Phe	Asp	Thr	Tyr	Glu	Leu	Lys	Asp	
			420				425					430				
cgg	gtg	acc	tac	ttt	gac	cgc	aac	tat	ggg	ctt	cgc	aca	ttc	ctg	ttc	1345
Arg	Val	Thr	Tyr	Phe	Asp	Arg	Asn	Tyr	Gly	Leu	Arg	Thr	Phe	Leu	Phe	

435	440	445	
tgc acg ccg ttc acg ccg gat	ggg cgc gca cac	ggg gag ctg ccc gag	1393
Cys Thr Pro Phe Thr Pro Asp	Gly Arg Ala His	Gly Glu Leu Pro Glu	
450	455	460	
caa cac aag cgt aag acg ctg	ctc agc acc gac cac gcc	ttc ccc tac	1441
Gln His Lys Arg Lys Thr Leu	Leu Ser Thr Asp His Ala	Phe Pro Tyr	
465	470	475 480	
atc aag act cgc atc cgt gtg	tgc cac cgg gag gag acg	gtg ctg acg	1489
Ile Lys Thr Arg Ile Arg Val	Cys His Arg Glu Glu Thr	Val Leu Thr	
485	490	495	
cca gtg gag gtg gcc atc gag	gac atg cag aag aag aca	cgg gag ctg	1537
Pro Val Glu Val Ala Ile Glu	Asp Met Gln Lys Lys Thr	Arg Glu Leu	
500	505	510	
gcc ttt gcc acc gag cag gac	cca cca gat gct aag atg	cta cag atg	1585
Ala Phe Ala Thr Glu Gln Asp	Pro Pro Asp Ala Lys Met	Leu Gln Met	
515	520	525	
gtg ctt cag ggc tct gta ggg	ccc acc gtg aac cag ggt	ccc ctg gag	1633
Val Leu Gln Gly Ser Val Gly	Pro Thr Val Asn Gln Gly	Pro Leu Glu	
530	535	540	
gtg gcc cag gtg ttt tta gca	gag atc ccg gaa gac ccc	aag ctc ttc	1681
Val Ala Gln Val Phe Leu Ala	Glu Ile Pro Glu Asp Pro	Lys Leu Phe	
545	550	555 560	
cgg cat cac aac aaa ttg cgg	ctc tgc ttc aag gac ttc	tgc aag aaa	1729
Arg His His Asn Lys Leu Arg	Leu Cys Phe Lys Asp Phe	Cys Lys Lys	
565	570	575	
tgt gag gat gcg ctg cgg aaa	aat aag gcc ctg att ggg	ccg gac cag	1777
Cys Glu Asp Ala Leu Arg Lys	Asn Lys Ala Leu Ile Gly	Pro Asp Gln	
580	585	590	
aag gag tac cac cgt gag ctg	gag cgc aac tac tgc cgc	ctg cgg gag	1825
Lys Glu Tyr His Arg Glu Leu	Glu Arg Asn Tyr Cys Arg	Leu Arg Glu	
595	600	605	
gct ctg cag ccc ctg ctt acc	cag cgc ctg ccc cag ctg	atg gca ccc	1873
Ala Leu Gln Pro Leu Leu Thr	Gln Arg Leu Pro Gln Leu	Met Ala Pro	
610	615	620	
acc cca ccc ggc ctc agg aac	tcc ttg aac aga gca agt	ttc cga aag	1921
Thr Pro Pro Gly Leu Arg Asn	Ser Leu Asn Arg Ala Ser	Phe Arg Lys	
625	630	635 640	
gca gac ctc tga gccacaagg	accaaagctg tacctagagg	aaccagcacc	1973
Ala Asp Leu			
cgggcctcag ctgtctgtgc	tgcgagggga gtctgccctg	gtgccactg ggctgtgggg	2033
tgaccacaact gtacttgggg	ctgggcctc tgccctgtg	tccccatctg tgtgcactga	2093
tgcttccctcc cttttttaat	ttaaaatggt ttttataagc	aaaaaaaaa aaaaaa	2149

<211> 643
 <212> PRT
 <213> Homo sapiens
 <223> preliminary human CLASP-7 cDNA sequence

<400> 60

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Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Asp Leu Leu Lys Val Val
 1             5             10             15

Leu Tyr Ser Leu Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly
          20             25             30

Leu Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe
          35             40             45

Glu Glu Asp Thr Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg
          50             55             60

His Cys Gly Ser Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser
          65             70             75             80

Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala
          85             90             95

Arg Val Lys Met Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr
          100            105            110

Thr Gln Asn Phe Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile
          115            120            125

Leu Thr Tyr Ala Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala
          130            135            140

Glu Gln Val Gln Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp
          145            150            155            160

Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp
          165            170            175

Leu Met Tyr Arg Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg
          180            185            190

Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn
          195            200            205

His Ala Glu Ala Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala
          210            215            220

Glu Tyr Leu Ala Leu Leu Glu Asp His Arg His Leu Pro Val Gly Cys
          225            230            235            240

Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile
          245            250            255

Ser Asp Asp Ile Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys
          260            265            270

His Phe Thr Glu Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly
          275            280            285

Tyr Phe Thr Met Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys

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290	295	300
Asn Leu Ile Pro Ile	Leu Glu Ala His Arg	Asp Tyr Lys Lys Leu Ala
305	310	315 320
Ala Val His Gly Lys	Leu Gln Glu Ala Phe Thr	Lys Ile Met His Gln
	325	330 335
Ser Ser Gly Trp Glu	Arg Val Phe Gly Thr Tyr Phe	Arg Val Gly Phe
	340	345 350
Tyr Gly Ala His Phe	Gly Asp Leu Asp Glu Gln Glu	Phe Val Tyr Lys
	355	360 365
Glu Pro Ser Ile Thr	Lys Leu Ala Glu Ile Ser His	Arg Leu Glu Glu
	370	375 380
Phe Tyr Thr Glu Arg	Phe Gly Asp Asp Val Val	Glu Ile Ile Lys Asp
	385	390 395 400
Ser Tyr Pro Val Asp	Lys Ser Lys Leu Asp Ser	Gln Lys Ala Tyr Ile
	405	410 415
Gln Ile Thr Tyr Val	Glu Pro Tyr Phe Asp Thr	Tyr Glu Leu Lys Asp
	420	425 430
Arg Val Thr Tyr Phe	Asp Arg Asn Tyr Gly Leu	Arg Thr Phe Leu Phe
	435	440 445
Cys Thr Pro Phe Thr	Pro Asp Gly Arg Ala His	Gly Glu Leu Pro Glu
	450	455 460
Gln His Lys Arg Lys	Thr Leu Leu Ser Thr Asp	His Ala Phe Pro Tyr
	465	470 475 480
Ile Lys Thr Arg Ile	Arg Val Cys His Arg Glu	Glu Thr Val Leu Thr
	485	490 495
Pro Val Glu Val Ala	Ile Glu Asp Met Gln Lys	Lys Thr Arg Glu Leu
	500	505 510
Ala Phe Ala Thr Glu	Gln Asp Pro Pro Asp Ala	Lys Met Leu Gln Met
	515	520 525
Val Leu Gln Gly Ser	Val Gly Pro Thr Val Asn	Gln Gly Pro Leu Glu
	530	535 540
Val Ala Gln Val Phe	Leu Ala Glu Ile Pro Glu	Asp Pro Lys Leu Phe
	545	550 555 560
Arg His His Asn Lys	Leu Arg Leu Cys Phe Lys	Asp Phe Cys Lys Lys
	565	570 575
Cys Glu Asp Ala Leu	Arg Lys Asn Lys Ala Leu	Ile Gly Pro Asp Gln
	580	585 590
Lys Glu Tyr His Arg	Glu Leu Glu Arg Asn Tyr	Cys Arg Leu Arg Glu
	595	600 605
Ala Leu Gln Pro Leu	Leu Thr Gln Arg Leu Pro	Gln Leu Met Ala Pro
	610	615 620

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<210> 61
<211> 120
<212> DNA
<213> Homo sapiens
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ccgcgccttc gcgcacaaga tcaacaggta gtgtggccgc gggggccccc cccacctccc 120
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<210> 62
<211> 141
<212> DNA
<213> Homo sapiens
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<220>
<223> exon 72530-72670

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<400> 62
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ccgggaacgc agtggctccc cccactccag caggcgctgc agcagctccc tgggggtaag 120
tatttggggg gtccgcccc a                                     141
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<210> 63
<211> 231
<212> DNA
<213> Homo sapiens
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<220>
<223> exon 73300-73530

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tgaggatgta cttctgagcc ggccaccaga tgctgagccc gggcccttca gggacctggt 120
agaattccca gctgatgact ttgagcttgc gctgcagccc cgggaatgcc ggaccacgga 180
gcccgggatc cccaaggatg agtgggttca gccccacgcc ctctctgcct g 231
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<210> 64
<211> 131
<212> DNA
<213> Homo sapiens
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<220>
<223> exon 73700-73830
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ggtaggagatg tatattgagg actgggtcat tgtccacaga aggtgagtct gacttagggg 120
cagctcaggg g                                     131
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<210> 65
 <211> 181
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 74010-74190

<400> 65
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 ccacagacac acagcgggag cgacagaagg gcctcccccg ccagggtcttt gagcaggatg 120
 cttctggaga cgagaggtcc ggccctgagg actcgggtgag gaagccccctg gctgggggtca 180
 c 181

<210> 66
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 75170-75450

<400> 66
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 gacacccctc gaagcagtgg tgcctctagc atcttcgacc tgaggaacct ggcagctgac 120
 tcattgtctg cctctctgct agagcgggag gccccagaag atgtggaccg gcgcaatgaa 180
 acccttcgac ggcagcaccg gccccgggcc ctgctcacc tctaccggc acctgacgag 240
 gtgggtgccc cttcccagat atcagccaac cagcatttac t 281

<210> 67
 <211> 151
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 78100-78250

<400> 67
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 cagagccacc ccgcgagcac tttggacaaa ggatcttggc caagtgtctg tcgctcaagt 120
 gagtatactg acatgtctct cttcttagat g 151

<210> 68
 <211> 121
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 80380-80500

<400> 68
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 tggctctgta tgatgtgcgg gagaaaaaga aggtaggagg cccttttttc tctttcctcc 120
 c 121

<210> 69
 <211> 211
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 80540-80750

<400> 69
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 ctccgactcc atgaaggggc tgcttcgggc tcatggcacc caccctgccca tctccaccct 120
 ggcccgtctt gccatcttct ctgtgacctt cccctcacct gacatcttcc tggatcatcaa 180
 ggtgcctgct ggggctgggc aagggggtgg t 211

<210> 70
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 82370-82510

<400> 70
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 cagtgaagtgc tgtgagcctt acatgggtgtt gaaagaagtg gacacagcca aggtaagcgt 120
 gtggaggctg gactaggggc a 141

<210> 71
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 82540-82760

<400> 71
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 ctggcggccg agcagttctg caccgcctg ggccgctacc gcatgccctt cgctgggacg 120
 gccgtgcact tggccaacat cgtgagcagc gctgggcagc tggaccggga ctctgactcg 180
 gagggcggtg aggaggcggg gctaacaggc ttggggcggg g 221

<210> 72
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 82860-83060

<400> 72
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 ccgccgccgt cggggggcccc aggaccgggc gagttagtggg gacgacgcct gcagcttctc 120
 tggcttccgt ccagccacgc taactgtcac aaacttcttt aagcaggtgt cctaccctgg 180
 ggccaggagac tctcccactc c 201

<210> 73
 <211> 161

<212> DNA
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<220>
 <223> exon 83100-83260

<400> 73
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 cttcaagttc ctggctgaca tgaggcgccc gtcgtccctg ctgcggcgac tacgtcctgt 120
 gactggtgcg tggcacaccc catacacaag aagtatcact c 161

<210> 74
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 84050-84270

<400> 74
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 aaatccccac ttctgcctct cccctgagct gcttcatatc aagccctacc cggaccccag 120
 gggccggccc accaaggaga ttctggagtt ccccgcccgc gaagtctatg cccccatac 180
 cagctacagg tacggcctct ggggcccagc tgggcacttg a 221

<210> 75
 <211> 191
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 87940-88130

<400> 75
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 gcacagcctc aacttcagca gccgccaggg ctccgtgcgc aaccttgctg tgcgagtga 120
 gtacatgaca ggcgaggacc ccagccaggg tctgccggtc agtggctgtg cccagggaa 180
 ggggggtagg g 191

<210> 76
 <211> 131
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 88140-88270

<400> 76
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 taccgcgag gccttcacac cgggtggtcta ccataacaag tatgtagggg gacacgtgag 120
 gaacttgagg g 131

<210> 77
 <211> 211
 <212> DNA
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<220>

<223> exon 88470-88680

<400> 77

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gccccccagca gatccccccag cccgattctg ccaggtcccc cgagttctac gaggagtcca 60
agctgcatctt tccagcctgc gtgacagaga accatcacct gctgttcacc ttctaccatg 120
tcagctgcca gccccggcgg ggcactgccc tggagacacc cgtgggcttt actgtgagcc 180
gtccccctccc tccctcccc tgagccctcc t                                     211

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<210> 78

<211> 191

<212> DNA

<213> Homo sapiens

<220>

<223> exon 88680-88870

<400> 78

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tcgtccccca acctggccgc agacctgacc tccagcctct cccagtgga tcccactgct 60
gcagcacggg cgctgagga cgggccctt ctgtctccca gtgtctgtgg accagccgcc 120
gccagctat tccgtgctca caccgatgt atgtgccctg gagctcctgc ctgccaatgc 180
actgtcccca g                                     191

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<210> 79

<211> 171

<212> DNA

<213> Homo sapiens

<220>

<223> exon 89360-89530

<400> 79

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cagggagggc tgaccagtgc ccacctggtg cctccctccc acaggtggcg cttccgggca 60
tgcgctgggt ggacggtcac aaggcggtgt tcagtgtgga gtcacagcc gtgtcctctg 120
tgcaccccca ggtacggggt gggccgggaa ccaagagtcc cgccctgctc c                                     171

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<210> 80

<211> 321

<212> DNA

<213> Homo sapiens

<220>

<223> exon 89660-89980

<400> 80

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ttcattccct gaggccccac cctgctcact ccacatccct acccaggacc cctacctgga 60
caaattcttc accctgggtgc acgtcctgga ggaggagacc ttccattcc ggctcaagga 120
cactgtgctg agcgagggca acgtggagca ggagctgcgg gccagtcttg cagcactgcg 180
cctggccagc cccgaacccc ttgtggcctt ctcccaccac gtgctggaca agctcgtgcg 240
tctggtcatc aggcccccca tcatcagtgg ccagattggt aagcgaatgt ggcctcagac 300
ctcagtttcc ccatccacat g                                     321

```

<210> 81

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<223> exon 90480-97030

<400> 81

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agcctttgaa gcaatggccc atgtagtcag ccttggtcac cggagcctgg aggcagccca 120
ggatgcccgc ggtcactgcc cacagctggc tgcctacgct cactacgctt ttgccttcc 180
tggcactgag cccagcctcc cggatggtga gttttagtaa atccctgtga gacgagaaat 240
atctgggaga a 251
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<210> 82

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<223> exon 92870-93120

<400> 82

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gacagtgcag gctgccacac tggcccgtgg ctctggtcgc cccgcaagcc tctacctggc 120
gcgttccaag agcatcagca gcagcaaccc tgacctcgcc gtggcccctg gctctgtgga 180
tgacgaggtt tcccgcaccc tggccagcaa ggtaggggcaa cggggggcct ggaatctcca 240
gcctcagtg t 251
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<210> 83

<211> 181

<212> DNA

<213> Homo sapiens

<220>

<223> exon 97210-97390

<400> 83

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tgcaagtgggt ggtcagcagc agtgccgtac gcgaggccat cctccagcac gcctggttct 120
tcttccagct catggtgaga cccctcctc cctgcctggt ggcaagagac cccagtgga 180
g 181
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<210> 84

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<223> exon 98770-98990

<400> 84

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ctgcttgccc agcgactaga cacacccgc aagctgcgct tccccggacg cttcctggac 120
gacatcactg ccttggtggg ctctgtgggc ctggagggtca tcaccgtgt ccacaagggtg 180
agagatgcag ggtctcaatg tgggaagaaa cctgaggggag g 221
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<210> 85

<211> 211

<212> DNA

<213> Homo sapiens

<220>

<223> exon 103130-103340

<400> 85

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ggggctgagg tttgggtgtg tgggttgaca ggcacctgtg tccccaggat gtggagctgg 60
ccgagcacct caacgccagc ctggctttct tcctcagtga ctttctgtcc ctgggtggacc 120
ggggctttgt cttcagcctg gtccggggccc actacaagca ggtaggagtg ggcgtgggca 180
gggtgggcat ggcattggat gaaggcggag c 211

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<210> 86

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<223> exon 103340-103590

<400> 86

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caatgttgac atcactgatg gccaccctc tcctgcaggt ggccacgcgg ctccagtcgt 60
cccctaattc agcagccctg ctgaccctgc gcatggaatt caccgcctc ctgtgcagcc 120
acgagcacta cgtgaccctc aacctccctt gctgccccct gtcacctcca gcctcgccct 180
ccccctctgt gtcctccacc acctcccagg tgggctgcct tcacttctgc ctctctctt 240
tgacctacaa c 251

```

<210> 87

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<223> exon 103990-104220

<400> 87

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agccaagccc cggaccccaa ggtgaccagc atgttcgaac tgagtggacc attccggcag 120
cagcacttcc tagctgggct cctgctgacg gagctggcac tggccctcga acctgaggct 180
gaaggggtgag cagagctcct gtctagcccc aggacagggt ggacagtcca g 231

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<210> 88

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<223> exon 104220-104480

<400> 88

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agaaggccat cagtgtgtg cacagcctgc tatgtggcca tgacctgac ccccgctacg 120
ccgaggccac tgtgaaggct cgtgtggccg agctgtacct gccactgcta tcgattgcac 180
gggatacctt gccacggctg catgactttg ctggtcagtg ggccagggga agatggggtc 240
acatgatcca gggacttggt c 261

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<210> 89

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<223> exon 108850-109100

<400> 89

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caagactggc ctcaatgctt gactcagaca cagaaggcga aggggacatt gcgggtacca 120
tcaacccctc tgtggccatg gccattgctg gtggcccccct agcccctggc tcccgggcca 180
gcatctccca ggggccacca acggtgagta gggaggcttg tccccataga catcatccac 240
tttgaatgag a 251

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<210> 90

<211> 271

<212> DNA

<213> Homo sapiens

<220>

<223> exon 109140-109410

<400> 90

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gctgtgccct ctctgctgag tcaagccgga ccttgctggc gtgtgtgctg tgggtgctga 120
aaaacaccga gccggcgctc ctgcagcgtc gggccactga cctgacactc cccagctgg 180
gacgtctgtt ggatttctg tacctttgcc tagctgcctt tgagtacaag gtttgagggc 240
gtgggcagga gatgatggag gaggcaggct a 271

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<210> 91

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<223> exon 110310-110530

<400> 91

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gaaaagagca gagtcagcct ggaaccccag ttctctgcac ccccagggga aaaaggcctt 60
tgaacgcata aacagcctca cattcaaaaa atctctggat atgaaggcgc ggctagagga 120
agccattctg ggtaccatcg gagctcgaca agaaatgggt cggcgaagtc gtggaagag 180
ggtgacatac ccacgtgtcc ccatcccacc agctgctccc a 221

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<210> 92

<211> 171

<212> DNA

<213> Homo sapiens

<220>

<223> exon 110770-110940

<400> 92

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tgtgttttta cgcattctgtg atcgtgcacc cacgcgtctc agagaggagc ccgtttggga 60
atccggagaa tgtgcgctgg cggaagagcg tcacacactg gaagcaaaacc tcagaccgcg 120
tggacaagta ggtgtgggca ggagggtgtc tgctgagttc agaacagttt g 171

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<210> 93

<211> 181

<212> DNA

<213> Homo sapiens

<220>

<223> exon qq590-111770

<400> 93

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gaacacgagg ccttggtgga agggaaacctg gcaaccgagg caagcctagt gggtctggac 120
acactggaga tcacgtgca ggtagggctt gatccagcat ctgccttggtg ctctgagccc 180
a 181
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<210> 94

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<223> exon 111830-112050

<400> 94

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aagcccggga gagcgtcttg ggggcagtgc tgaaggttgt gctgtacagc ctgggcagtg 120
cccagagtgc cctcttcttg cagcatggcc tggccaccca gagggccctt gtgtccaagg 180
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<210> 95

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<223> exon 112910-113140

<400> 95

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aacggggagg ggctggacag tgtctgtctg ggtccttggg ggcagttccc ggagctgctg 60
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agccgcatca gcaccatccg cagcgacgcc agcgctcgc tgtacctgct catgcgacag 180
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c 241
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<210> 96

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<223> exon 114090-114340

<400> 96

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cacctgcgac gttcactcaa aaccatcctc acctatgctg aggaggacat ggggctgcgg 180
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taactcccaa c 251
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 gcacatgata ctgacggaca cgggtgaagat gaaggaacac caggaggacc ctgagatgct 120
 catcgacctc atgtacaggt gaggtggggc agctggcacc ttcagccacg cccacgcccc 180
 a 181

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 gggcaaccac gccgaggccg cccagtgcac ggtgcacgcg gccgccctcg tggtgagta 180
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 gctccgggaa gcacttcact gagctggggc tggtaggggt gctggaacag gcagccggct 180
 acttcaccat ggtgaggcct tggggactgg gtgcaggaga gggggctcgg gccagggagg 240
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<220>
 <223> exon 121670-121900

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 aagctggccg cgggtgcacg caaactgcag gaggccttca ccaagatcat gcaccagggtg 180
 ggcccaggac cccctcccca gacccaccc tcagccccac tctcatcc 229

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<211> 91
 <212> DNA
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<220>
 <223> exon 121910-122000

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 gtcagccttg gtggacagcc acctgcctct g 91

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<220>
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<220>
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 <212> DNA
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<220>
 <223> putative human CLASP-7 promoter region

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 tacaaaaaat tagccagggtg tgatgggtggg tgccctgtaat cccagctact cgggaggctg 180
 aggcaggaga atcgcttgaa cctgggaggc agagggtgcg gtgagccgag attgtgccat 240
 tgcactccag tctggggcaac aagagcgaaa tgccacctca aaataaataa ataaataaat 300
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 gggaatgaga acagcacgtg caaaggccct gaggcagagc cacggccttg tctgattcaa 420
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 acctgccggt gcagaggcat gcagggtgaga aaggggtgag ctctccaga ggggagtgct 540
 ggctggagaa ttctctaaaa atgctgcagc agtgctggga gagaggccag tggggagaga 600
 tttgagacca tagattaacc aagacatccc cacctcttcc tcttggtaga ggcggccccc 660

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gtcaccagg ctggattgaa atggcacaat cacagctcac tgcagccttg acctcccagg 1020
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<211> 2008

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-4

<400> 105

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Ser Leu Phe Val Lys Glu Cys Ile Lys Thr Tyr Ser Thr Asp Trp His
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Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
          50             55             60

Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
          65             70             75             80

Ile Asp Glu Asp Cys Glu Lys Asp Glu Asp Ser Ser Ser Leu Cys Ser
          85             90             95

Gln Lys Gly Gly Val Ile Lys Gln Gly Trp Leu His Lys Ala Asn Val
          100            105            110

Asn Ser Thr Ile Thr Val Thr Met Lys Val Phe Lys Arg Arg Tyr Phe
          115            120            125

Tyr Leu Thr Gln Leu Pro Asp Gly Ser Tyr Ile Leu Asn Ser Tyr Lys
          130            135            140

Asp Glu Lys Asn Ser Lys Glu Ser Lys Gly Cys Ile Tyr Leu Asp Ala

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145		150		155		160
Cys Ile Asp Val Val Gln Cys Pro Lys Met Arg Arg His Ala Phe Glu						
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Leu Lys Met Leu Asp Lys Tyr Ser His Tyr Leu Ala Ala Glu Thr Glu						
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Gln Glu Met Glu Glu Trp Leu Ile Thr Leu Lys Lys Ile Ile Gln Ile						
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Asn Thr Asp Ser Leu Val Gln Glu Lys Lys Glu Thr Val Glu Thr Ala						
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Gln Asp Asp Glu Thr Ser Ser Gln Gly Lys Ala Glu Asn Ile Met Ala						
		225		230		235
Ser Leu Glu Arg Ser Met His Pro Glu Leu Met Lys Tyr Gly Arg Glu						
		245		250		255
Thr Glu Gln Leu Asn Lys Leu Ser Arg Gly Asp Gly Arg Gln Asn Leu						
		260		265		270
Phe Ser Phe Asp Ser Glu Val Gln Arg Leu Asp Phe Ser Gly Ile Glu						
		275		280		285
Pro Asp Ile Lys Pro Phe Glu Glu Lys Cys Asn Lys Arg Phe Leu Val						
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Asn Cys His Asp Leu Thr Phe Asn Ile Leu Gly Gln Ile Gly Asp Asn						
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Ala Lys Gly Pro Pro Thr Asn Val Glu Pro Phe Phe Ile Asn Leu Ala						
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Leu Phe Asp Val Lys Asn Asn Cys Lys Ile Ser Ala Asp Phe His Val						
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Asp Leu Asn Pro Pro Ser Val Arg Glu Met Leu Trp Gly Ser Ser Thr						
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Gln Leu Ala Ser Asp Gly Ser Pro Lys Gly Ser Ser Pro Glu Ser Tyr						
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Ile His Gly Ile Ala Glu Ser Gln Leu Arg Tyr Ile Gln Gln Gly Ile						
		385		390		395
Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile						
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Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile						
		420		425		430
Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala						
		435		440		445
Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp						
		450		455		460
Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp						
		465		470		475
						480

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Glu	Asp	Ile	Leu	Lys	Leu	Leu	Ser	Glu	Tyr	Lys	Lys	Pro	Glu	Lys	Thr		
			500					505					510				
Lys	Leu	Gln	Ile	Ile	Pro	Gly	Gln	Leu	Asn	Ile	Thr	Val	Glu	Cys	Val		
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Pro	Val	Asp	Leu	Ser	Asn	Cys	Ile	Thr	Ser	Ser	Tyr	Val	Pro	Leu	Lys		
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Pro	Phe	Glu	Lys	Asn	Cys	Gln	Asn	Ile	Thr	Val	Glu	Val	Glu	Glu	Phe		
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His	Leu	Tyr	Val	Tyr	Pro	Leu	Gln	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Thr		
			580					585					590				
Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Val	Cys	Val	Glu	Phe	Arg	Asp	Ser		
		595					600					605					
Asp	Glu	Ser	Asp	Ala	Ser	Ala	Leu	Lys	Cys	Ile	Tyr	Gly	Lys	Pro	Ala		
	610					615					620						
Gly	Ser	Val	Phe	Thr	Thr	Asn	Ala	Tyr	Ala	Val	Val	Ser	His	His	Asn		
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Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Ile	His		
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Leu	His	Gln	Lys	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys		
		660						665					670				
Glu	Ile	Asn	Thr	Lys	Gly	Thr	Thr	Lys	Lys	Gln	Asp	Thr	Val	Glu	Thr		
	675						680					685					
Pro	Val	Gly	Phe	Ala	Trp	Val	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Ile	Ile		
	690					695					700						
Thr	Phe	Glu	Gln	Gln	Leu	Pro	Val	Ser	Ala	Asn	Leu	Pro	Pro	Gly	Tyr		
705					710					715				720			
Leu	Asn	Leu	Asn	Asp	Ala	Glu	Ser	Arg	Arg	Gln	Cys	Asn	Val	Asp	Ile		
			725					730						735			
Lys	Trp	Val	Asp	Gly	Ala	Lys	Pro	Leu	Leu	Lys	Phe	Lys	Ser	His	Leu		
		740						745					750				
Glu	Ser	Thr	Ile	Tyr	Thr	Gln	Asp	Leu	His	Val	His	Lys	Phe	Phe	His		
		755					760					765					
His	Cys	Gln	Leu	Ile	Gln	Ser	Gly	Ser	Lys	Glu	Val	Pro	Gly	Glu	Leu		
	770					775					780						
Ile	Lys	Tyr	Leu	Lys	Cys	Leu	His	Ala	Met	Glu	Ile	Gln	Val	Met	Ile		
785					790					795					800		

Gln Phe Leu Pro Val Ile Leu Met Gln Leu Phe Arg Val Leu Thr Asn
 805 810 815
 Met Thr His Glu Asp Asp Val Pro Ile Asn Cys Thr Met Val Leu Leu
 820 825 830
 His Ile Val Ser Lys Cys His Glu Glu Gly Leu Asp Ser Tyr Leu Arg
 835 840 845
 Ser Phe Ile Lys Tyr Ser Phe Arg Pro Glu Lys Pro Ser Ala Pro Gln
 850 855 860
 Ala Gln Leu Ile His Glu Thr Leu Ala Thr Thr Met Ile Ala Ile Leu
 865 870 875 880
 Lys Gln Ser Ala Asp Phe Leu Ser Ile Asn Lys Leu Leu Lys Tyr Ser
 885 890 895
 Trp Phe Phe Phe Glu Ile Ile Ala Lys Ser Met Ala Thr Tyr Leu Leu
 900 905 910
 Glu Glu Asn Lys Ile Lys Leu Pro Arg Gly Gln Arg Phe Pro Glu Thr
 915 920 925
 Tyr His His Val Leu His Ser Leu Leu Leu Ala Ile Ile Pro His Val
 930 935 940
 Thr Ile Arg Tyr Ala Glu Ile Pro Asp Glu Ser Arg Asn Val Asn Tyr
 945 950 955 960
 Ser Leu Ala Ser Phe Leu Lys Arg Cys Leu Thr Leu Met Asp Arg Gly
 965 970 975
 Phe Ile Phe Asn Leu Ile Asn Asp Tyr Ile Ser Gly Phe Ser Pro Lys
 980 985 990
 Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe Glu Phe Leu Gln Thr Ile
 995 1000 1005
 Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met Ala Phe Ala
 1010 1015 1020
 Lys Pro Lys Leu Gln Arg Val Gln Asp Ser Asn Leu Glu Tyr Ser Leu
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 Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg
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 Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg
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 Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro
 1090 1095 1100
 Phe Val Gly Leu Leu Leu Glu Asn Ile Gln Arg Leu Ala Gly Arg Asp
 1105 1110 1115 1120
 Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu

1125	1130	1135
Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr 1140	1145	1150
Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys 1155	1160	1165
Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe 1170	1175	1180
Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr Arg Gln Ser Ser Thr Arg 1185	1190	1195
Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp Gln Tyr Glu Ile Arg Ser 1205	1210	1215
Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys Met Ile Ser Glu Asp Thr 1220	1225	1230
Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile 1235	1240	1245
Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys 1250	1255	1260
Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly 1265	1270	1275
Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly 1285	1290	1295
Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe 1300	1305	1310
Thr Leu Asn His Ser Ser Thr Thr Thr Glu Ala Asp Ile Phe His Gln 1315	1320	1325
Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu Val Ser Leu Thr Val Leu 1330	1335	1340
Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe Lys Thr Gln Leu Leu Asn 1345	1350	1355
Asn Asp Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Ile His Leu 1365	1370	1375
Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe 1380	1385	1390
Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe Pro Ser Ala Phe Phe Lys 1395	1400	1405
Gly Arg Val Asn Met Cys Ala Ala Phe Cys Tyr Glu Val Leu Lys Cys 1410	1415	1420
Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu 1425	1430	1435
Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe 1445	1450	1455

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 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
 1505 1510 1515 1520
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 Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu
 1540 1545 1550
 Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly
 1555 1560 1565
 Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val
 1570 1575 1580
 Ala Glu Phe Leu His Arg Lys Lys Leu Phe Pro Asn Gly Cys Ser Ala
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 Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu
 1605 1610 1615
 Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu
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 Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu
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 1765 1770 1775

Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn
 1780 1785 1790
 His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly
 1795 1800 1805
 Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu
 1810 1815 1820
 Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn
 1825 1830 1835 1840
 Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Gly Ala Thr Asp Glu
 1845 1850 1855
 Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys Leu Cys Ser Ser Thr Asp
 1860 1865 1870
 Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val
 1875 1880 1885
 Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp
 1890 1895 1900
 Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
 1905 1910 1915 1920
 Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn
 1925 1930 1935
 Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys
 1940 1945 1950
 Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu
 1955 1960 1965
 Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr
 1970 1975 1980
 Leu His Val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr
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 Gly Ser Pro Arg Tyr Ala Glu Val
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<220>
 <223> human CLASP-5

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 35 40 45
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 50 55 60
 Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr
 65 70 75 80
 Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu
 85 90 95
 Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg
 100 105 110
 His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala
 115 120 125
 Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn
 130 135 140
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 145 150 155 160
 Ala Arg Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser
 165 170 175
 Val Asp Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro
 180 185 190
 Lys Glu His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys
 195 200 205
 Phe Glu Ile Glu Ile Glu Pro Leu Phe Ala Ser Ile Ala Leu Tyr Asp
 210 215 220
 Val Lys Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn
 225 230 235 240
 Ser Asp Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala
 245 250 255
 Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser
 260 265 270
 Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly
 275 280 285
 Asp Ile Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp
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 Gly Gly Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu
 305 310 315 320
 Ser Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala
 325 330 335
 Pro Ile Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu
 340 345 350
 Val Thr Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg

355					360					365					
Arg	Thr	Leu	Ala	Gln	Ser	Arg	Arg	Leu	Ser	Glu	Arg	Ala	Leu	Ser	Leu
370					375					380					
Glu	Glu	Asn	Gly	Val	Gly	Ser	Asn	Phe	Lys	Thr	Ser	Thr	Leu	Ser	Val
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Ser	Ser	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu	Ser	Asp	Glu	Asp	Leu
405					410					415					
Phe	Lys	Phe	Leu	Ala	Asp	Tyr	Lys	Arg	Ser	Ser	Ser	Leu	Gln	Arg	Arg
420					425					430					
Val	Lys	Ser	Ile	Pro	Gly	Leu	Leu	Arg	Leu	Glu	Ile	Ser	Thr	Ala	Pro
435					440					445					
Glu	Ile	Ile	Asn	Cys	Cys	Leu	Thr	Pro	Glu	Met	Leu	Pro	Val	Lys	Pro
450					455					460					
Phe	Pro	Glu	Asn	Arg	Thr	Arg	Pro	His	Lys	Glu	Ile	Leu	Glu	Phe	Pro
465					470					475					480
Thr	Arg	Glu	Val	Tyr	Val	Pro	His	Thr	Val	Tyr	Arg	Asn	Leu	Leu	Tyr
485					490					495					
Val	Tyr	Pro	Gln	Arg	Leu	Asn	Phe	Val	Asn	Lys	Leu	Ala	Ser	Ala	Arg
500					505					510					
Asn	Ile	Thr	Ile	Lys	Ile	Gln	Phe	Met	Cys	Gly	Glu	Asp	Ala	Ser	Asn
515					520					525					
Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Gly	Pro	Glu	Phe	Leu	Gln
530					535					540					
Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr
545					550					555					560
Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His
565					570					575					
Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala
580					585					590					
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn
595					600					605					
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys
610					615					620					
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln
625					630					635					640
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile
645					650					655					
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu
660					665					670					
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro
675					680					685					

Ile Arg Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu
 690 695 700
 Leu Lys Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu
 705 710 715 720
 Val Leu Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val
 725 730 735
 Gln Pro Met Val Ile Ala Gly Gln Thr Ala Asn Phe Ser Gln Phe Ala
 740 745 750
 Phe Glu Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp
 755 760 765
 Leu Ser Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val
 770 775 780
 His Tyr Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser
 785 790 795 800
 Gly Ala Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly
 805 810 815
 Arg Thr Ser Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val
 820 825 830
 Met Ser Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp
 835 840 845
 Glu Glu Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys
 850 855 860
 Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser
 865 870 875 880
 Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu
 885 890 895
 Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln
 900 905 910
 His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe
 915 920 925
 Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr
 930 935 940
 Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln
 945 950 955 960
 Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu
 965 970 975
 Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys
 980 985 990
 Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met
 995 1000 1005

Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn
 1010 1015 1020
 Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys
 1025 1030 1035 1040
 Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp
 1045 1050 1055
 Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln
 1060 1065 1070
 His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp
 1075 1080 1085
 Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala
 1090 1095 1100
 Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys
 1105 1110 1115 1120
 Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly
 1125 1130 1135
 Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
 1140 1145 1150
 Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
 1155 1160 1165
 Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
 1170 1175 1180
 Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
 1185 1190 1195 1200
 Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
 1205 1210 1215
 Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
 1220 1225 1230
 Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
 1235 1240 1245
 Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
 1250 1255 1260
 Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
 1265 1270 1275 1280
 Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
 1285 1290 1295
 Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
 1300 1305 1310
 Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
 1315 1320 1325
 Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn

1330	1335	1340
Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile 1345	1350	1355 1360
Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly 1365	1370	1375
Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr 1380	1385	1390
Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe 1395	1400	1405
Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys 1410	1415	1420
His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser 1425	1430	1435 1440
Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala 1445	1450	1455
Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala 1460	1465	1470
Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg 1475	1480	1485
Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln 1490	1495	1500
Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn 1505	1510	1515 1520
Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro 1525	1530	1535
Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala 1540	1545	1550
Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His 1555	1560	1565
Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala 1570	1575	1580
Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr 1585	1590	1595 1600
Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu 1605	1610	1615
Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly 1620	1625	1630
Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu 1635	1640	1645
Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val 1650	1655	1660

Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
1665 1670 1675 1680

Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
1685 1690 1695

Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
1700 1705 1710

Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
1715 1720 1725

Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
1730 1735 1740

Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
1745 1750 1755 1760

Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
1765 1770 1775

Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu
1780 1785 1790

Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
1795 1800 1805

Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
1810 1815 1820

Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
1825 1830 1835 1840

Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
1845 1850 1855

Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr
1860 1865 1870

Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met
1875 1880 1885

Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly
1890 1895 1900

Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
1905 1910 1915 1920

Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe
1925 1930 1935

Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr
1940 1945 1950

Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys
1955 1960 1965

Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu
1970 1975 1980

Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His
1985 1990 1995 2000

Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
2005 2010 2015

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<211> 2090

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-3

<400> 107

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Ala Glu Val Arg Lys Gln Ile Ser Gly Gln Tyr Ser Gly Ser Pro Gln
20 25 30

Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr
35 40 45

Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
50 55 60

Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
65 70 75 80

Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
85 90 95

Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
100 105 110

Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile
115 120 125

Arg Lys Tyr His Lys Leu Gly Thr Gly Phe Asn Pro Asn Thr Leu Asp
130 135 140

Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro Lys Gln Val Phe Glu Ser
145 150 155 160

Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu
165 170 175

Lys Arg Arg Ser Met Ser Ile Asp Asp Thr Pro Arg Gly Ser Trp Ala
180 185 190

Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu Pro Asp Ala Leu Leu Pro
195 200 205

Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu Ile Asp Arg Gln Asn Asp
210 215 220

Asp Gln Arg Lys Ser Asn Arg His Lys Glu Leu Phe Ala Leu His Pro
225 230 235 240

Ser Pro Asp Glu Glu Glu Pro Ile Glu Arg Leu Ser Val Pro Asp Ile
 245 250 255
 Pro Lys Glu His Phe Gly Gln Arg Leu Leu Val Lys Cys Leu Ser Leu
 260 265 270
 Lys Phe Glu Ile Glu Ile Glu Pro Ile Phe Ala Ser Leu Ala Leu Tyr
 275 280 285
 Asp Val Lys Glu Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu
 290 295 300
 Asn Ser Glu Gln Met Lys Gly Leu Leu Arg Pro His Val Pro Pro Ala
 305 310 315 320
 Ala Ile Thr Thr Leu Ala Arg Ser Ala Ile Phe Ser Ile Thr Tyr Pro
 325 330 335
 Ser Gln Asp Val Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln
 340 345 350
 Gly Asp Ile Gly Glu Cys Ala Glu Pro Tyr Met Ile Phe Lys Glu Ala
 355 360 365
 Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala
 370 375 380
 Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp
 385 390 395 400
 Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu
 405 410 415
 Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser
 420 425 430
 Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
 435 440 445
 Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
 450 455 460
 Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
 465 470 475 480
 Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
 485 490 495
 Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
 500 505 510
 Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
 515 520 525
 Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
 530 535 540
 Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
 545 550 555 560
 Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg

565										570					575				
Gln	Gly	Ser	Ala	Arg	Asn	Ile	Thr	Val	Lys	Val	Gln	Phe	Met	Tyr	Gly				
			580					585					590						
Glu	Asp	Pro	Ser	Asn	Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Cys				
		595					600					605							
Ser	Glu	Phe	Ser	Lys	Glu	Ala	Tyr	Thr	Ala	Val	Val	Tyr	His	Asn	Arg				
	610					615					620								
Ser	Pro	Asp	Phe	His	Glu	Glu	Ile	Lys	Val	Lys	Leu	Pro	Ala	Thr	Leu				
625					630					635					640				
Thr	Asp	His	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys	Gln				
				645					650					655					
Gln	Lys	Gln	Asn	Thr	Pro	Leu	Glu	Thr	Pro	Val	Gly	Tyr	Thr	Trp	Ile				
			660					665					670						
Pro	Met	Leu	Gln	Asn	Gly	Arg	Leu	Lys	Thr	Gly	Gln	Phe	Cys	Leu	Pro				
		675					680					685							
Val	Ser	Leu	Glu	Lys	Pro	Pro	Gln	Ala	Tyr	Ser	Val	Leu	Ser	Pro	Glu				
	690					695					700								
Val	Pro	Leu	Pro	Gly	Met	Lys	Trp	Val	Asp	Asn	His	Lys	Gly	Val	Phe				
705					710				715						720				
Asn	Val	Glu	Val	Val	Ala	Val	Ser	Ser	Ile	His	Thr	Gln	Asp	Pro	Tyr				
				725					730					735					
Leu	Asp	Lys	Phe	Phe	Ala	Leu	Val	Asn	Ala	Leu	Asp	Glu	His	Leu	Phe				
			740					745					750						
Pro	Val	Arg	Ile	Gly	Asp	Met	Arg	Ile	Met	Glu	Asn	Asn	Leu	Glu	Asn				
		755					760					765							
Glu	Leu	Lys	Ser	Ser	Ile	Ser	Ala	Leu	Asn	Ser	Ser	Gln	Leu	Glu	Pro				
	770					775					780								
Val	Val	Arg	Phe	Leu	His	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Leu	Leu	Val				
785					790					795					800				
Ile	Arg	Pro	Pro	Val	Ile	Ala	Gly	Gln	Ile	Val	Asn	Leu	Gly	Gln	Ala				
				805				810						815					
Ser	Phe	Glu	Ala	Met	Ala	Ser	Ile	Ile	Asn	Arg	Leu	His	Lys	Asn	Leu				
			820					825					830						
Glu	Gly	Asn	His	Asp	Gln	His	Gly	Arg	Asn	Ser	Leu	Leu	Ala	Ser	Tyr				
		835					840				845								
Ile	His	Tyr	Val	Phe	Arg	Leu	Pro	Asn	Thr	Tyr	Pro	Asn	Ser	Ser	Ser				
	850					855					860								
Pro	Gly	Pro	Gly	Gly	Leu	Gly	Gly	Ser	Val	His	Tyr	Ala	Thr	Met	Ala				
865					870					875					880				
Arg	Ser	Ala	Val	Arg	Pro	Ala	Ser	Leu	Asn	Leu	Asn	Arg	Ser	Arg	Ser				
				885					890					895					

Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp
 900 905 910
 Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn
 915 920 925
 Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn
 930 935 940
 Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn
 945 950 955 960
 Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr
 965 970 975
 Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln
 980 985 990
 Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala
 995 1000 1005
 Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr
 1010 1015 1020
 Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg
 1025 1030 1035 1040
 Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile
 1045 1050 1055
 Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr
 1060 1065 1070
 Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly
 1075 1080 1085
 Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys
 1090 1095 1100
 Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp
 1105 1110 1115 1120
 Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu
 1125 1130 1135
 Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser
 1140 1145 1150
 Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln
 1155 1160 1165
 Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His
 1170 1175 1180
 Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro
 1185 1190 1195 1200
 Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val
 1205 1210 1215

His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro
 1220 1225 1230
 Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile
 1235 1240 1245
 Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn
 1250 1255 1260
 Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu
 1265 1270 1275 1280
 Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr
 1285 1290 1295
 Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr
 1300 1305 1310
 Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu
 1315 1320 1325
 Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu
 1330 1335 1340
 Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
 1345 1350 1355 1360
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
 1365 1370 1375
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
 1380 1385 1390
 Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys

1540	1545	1550
Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr 1555	1560	1565
Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val 1570	1575	1580
Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln 1585	1590	1595 1600
Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr 1605	1610	1615
Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln 1620	1625	1630
Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val 1635	1640	1645
Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met 1650	1655	1660
Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp 1665	1670	1675 1680
Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu 1685	1690	1695
Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu 1700	1705	1710
Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe 1715	1720	1725
Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp 1730	1735	1740
Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr 1745	1750	1755 1760
Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser 1765	1770	1775
Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile 1780	1785	1790
Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His 1795	1800	1805
Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly 1810	1815	1820
Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr 1825	1830	1835 1840
Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala 1845	1850	1855
Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly 1860	1865	1870

Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885

Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900

Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920

Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935

Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950

Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965

Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980

Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala
 1985 1990 1995 2000

Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln
 2005 2010 2015

Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln
 2020 2025 2030

Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His
 2035 2040 2045

Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp
 2050 2055 2060

Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr
 2065 2070 2075 2080

Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro
 2085 2090

<210> 108

<211> 1980

<212> PRT

<213> Homo sapiens

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<223> human CLASP-2

<400> 108

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Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu
 20 25 30

Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp
 35 40 45

Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg
 50 55 60
 Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val
 65 70 75 80
 Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu
 85 90 95
 Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly
 100 105 110
 Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg
 115 120 125
 Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe
 130 135 140
 Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu
 145 150 155 160
 Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala
 165 170 175
 Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp
 180 185 190
 Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu
 195 200 205
 Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser
 210 215 220
 His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu
 225 230 235 240
 Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile
 245 250 255
 Lys Leu Lys Ser Glu Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp
 260 265 270
 Ala Gln Lys Leu Asp Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe
 275 280 285
 Glu Glu Lys Phe Gly Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser
 290 295 300
 Phe Asn Leu Gln Cys Cys Val Ala Glu Asn Glu Gly Pro Thr Thr
 305 310 315 320
 Asn Val Glu Pro Phe Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr
 325 330 335
 Asn Arg Lys Ile Ser Ala Asp Phe His Val Asp Leu Asn His Phe Ser
 340 345 350
 Val Arg Gln Met Leu Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser
 355 360 365

Gly Gln Ser Pro Ser Val Leu Lys Gly Ile Leu His Glu Ala Ala Met
 370 375 380
 Gln Tyr Pro Lys Gln Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp
 385 390 395 400
 Ile Phe Leu Val Ala Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr
 405 410 415
 His Cys Ala Glu Pro Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala
 420 425 430
 Gln Lys Val Leu Lys Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln
 435 440 445
 Tyr Arg Met Pro Phe Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala
 450 455 460
 Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln
 465 470 475 480
 Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp
 485 490 495
 Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn
 500 505 510
 Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val
 515 520 525
 Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys Thr
 530 535 540
 Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys His
 545 550 555 560
 Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro Lys
 565 570 575
 Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn Ile
 580 585 590
 Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln Pro
 595 600 605
 Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg Ser
 610 615 620
 Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp
 625 630 635 640
 Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu
 645 650 655
 Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser
 660 665 670
 Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu
 675 680 685
 Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro

690					695					700					
Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly
705					710					715					720
Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys
				725					730					735	
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln
			740					745					750		
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser
		755					760					765			
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu
	770					775					780				
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu
785						790					795				800
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala
			805						810					815	
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu
			820					825					830		
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys
		835					840					845			
Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu
	850					855					860				
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr
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Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile
				885					890					895	
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu
			900					905					910		
Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val
		915					920					925			
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro
	930					935					940				
Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg
945						950					955				960
Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn
				965					970					975	
Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr
			980					985					990		
Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro
		995					1000					1005			
Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln
	1010					1015					1020				

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 Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu
 1045 1050 1055
 Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu
 1060 1065 1070
 Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala
 1075 1080 1085
 Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn
 1090 1095 1100
 Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala
 1105 1110 1115 1120
 Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro
 1125 1130 1135
 Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys
 1140 1145 1150
 Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser
 1155 1160 1165
 Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu
 1170 1175 1180
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys
 1185 1190 1195 1200
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser
 1205 1210 1215
 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu
 1220 1225 1230
 Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
 1235 1240 1245
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
 1250 1255 1260
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
 1330 1335 1340

Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
1345 1350 1355 1360

Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His
1365 1370 1375

Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
1380 1385 1390

Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
1395 1400 1405

Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
1410 1415 1420

Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
1425 1430 1435 1440

Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
1445 1450 1455

Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
1460 1465 1470

Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly
1475 1480 1485

Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys
1490 1495 1500

Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
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Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
1525 1530 1535

Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
1540 1545 1550

Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
1555 1560 1565

Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
1570 1575 1580

Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
1585 1590 1595 1600

Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
1605 1610 1615

Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
1620 1625 1630

Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
1635 1640 1645

Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
1650 1655 1660

Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe

1665	1670	1675	1680
Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr	1685	1690	1695
Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys	1700	1705	1710
Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn	1715	1720	1725
Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val	1730	1735	1740
Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe	1745	1750	1755
Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr	1765	1770	1775
Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg	1780	1785	1790
Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile	1795	1800	1805
Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala	1810	1815	1820
Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser	1825	1830	1835
Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser	1845	1850	1855
Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe	1860	1865	1870
Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu	1875	1880	1885
Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu	1890	1895	1900
Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu	1905	1910	1915
Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile	1925	1930	1935
Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro	1940	1945	1950
Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr	1955	1960	1965
Met Val His Gly Met Thr Ser Ser Ser Ser Val Val	1970	1975	1980

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<220>

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<400> 109

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Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr
      35           40          45

Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
      50           55          60

Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
      65           70          75          80

Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
      85           90          95

Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala
      100          105          110

Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln
      115          120          125

Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu
      130          135          140

Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly
      145          150          155          160

Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser
      165          170          175

Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe
      180          185          190

Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu
      195          200          205

Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg
      210          215          220

Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu
      225          230          235          240

Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His
      245          250          255

Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile
      260          265          270

Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu
      275          280          285

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Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser
 290 295 300
 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr
 305 310 315 320
 Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile
 325 330 335
 Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser
 340 345 350
 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys
 355 360 365
 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys
 370 375 380
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His
 385 390 395 400
 Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp
 405 410 415
 Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
 420 425 430
 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
 435 440 445
 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
 450 455 460
 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
 465 470 475 480
 Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu
 485 490 495
 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
 500 505 510
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
 515 520 525
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
 530 535 540
 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
 545 550 555 560
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
 565 570 575
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
 580 585 590
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
 595 600 605

His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
 610 615 620
 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
 625 630 635 640
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
 645 650 655
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
 660 665 670
 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
 675 680 685
 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
 690 695 700
 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
 705 710 715 720
 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
 725 730 735
 Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
 740 745 750
 Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
 755 760 765
 Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
 770 775 780
 Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
 785 790 795 800
 Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His
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 Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu
 820 825 830
 Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser
 835 840 845
 Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala
 850 855 860
 Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser
 865 870 875 880
 Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp
 885 890 895
 Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu
 900 905 910
 Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu
 915 920 925
 Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu

930	935	940
His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe 945 950 955 960		
Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly 965 970 975		
Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His 980 985 990		
Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val 995 1000 1005		
Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val 1010 1015 1020		
Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu 1025 1030 1035 1040		
Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr 1045 1050 1055		
Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro 1060 1065 1070		
Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala 1075 1080 1085		
Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg 1090 1095 1100		
Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala 1105 1110 1115 1120		
Leu Gln Glu Asp Gln Asp Val Arg His Leu Ala Leu Ala Val Leu Lys 1125 1130 1135		
Asn Leu Met Ala Lys His Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg 1140 1145 1150		
Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu 1155 1160 1165		
Leu Asp Asn Met Pro Arg Ile Arg Leu His Asp Phe Ala Glu Gly Pro 1170 1175 1180		
Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr Glu Gly 1185 1190 1195 1200		
Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met Ala Ile 1205 1210 1215		
Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser Gln Gly 1220 1225 1230		
Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu Ser Ser 1235 1240 1245		
Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr Glu Pro 1250 1255 1260		

Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln Leu Gly
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 Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu Tyr Lys
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 Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys Lys Ser
 1300 1305 1310
 Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr Ile Gly
 1315 1320 1325
 Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro Phe Gly
 1330 1335 1340
 Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp Lys Gln
 1345 1350 1355 1360
 Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His Glu Ala
 1365 1370 1375
 Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val Leu Asp
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 Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala Arg Glu
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 Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr Glu Leu
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 Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser Arg Ile
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 Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu Met Arg
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 Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met Gln Val
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 Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln Asp Leu
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 Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met Lys Glu
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 His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala
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Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn
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 Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala Ala Gln
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 Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu
 1620 1625 1630
 Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile
 1635 1640 1645
 Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser
 1650 1655 1660
 Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly
 1665 1670 1675 1680
 Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly
 1685 1690 1695
 Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu
 1700 1705 1710
 Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu
 1715 1720 1725
 Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg
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 Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly
 1745 1750 1755 1760
 Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys
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 Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe
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 Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val Asp Lys
 1795 1800 1805
 Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu
 1810 1815 1820
 Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp
 1825 1830 1835 1840
 Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe Thr Pro
 1845 1850 1855
 Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg Lys Thr
 1860 1865 1870
 Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg Ile Arg
 1875 1880 1885
 Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val Ala Ile
 1890 1895 1900
 Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr Glu Gln

1905	1910	1915	1920
Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val			
1925		1930	1935
Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu			
1940		1945	1950
Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn Lys Leu			
1955		1960	1965
Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala Leu Arg			
1970		1975	1980
Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu			
1985		1990	1995
2000			
Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro Leu Leu			
2005		2010	2015
Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly Leu Arg			
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Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu			
35	40	45	
Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln			
50	55	60	
Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser			
65	70	75	80
Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His			
85	90	95	
Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser			
100	105	110	
Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile			
115	120	125	
Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His			

130	135	140
Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr		
145	150	155 160
Ser His Ser Ser Ser Lys Gly Gly Gly Gly Ala Gly Gly Thr Gly Val		
	165	170 175
Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn		
	180	185 190
Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr		
	195	200 205
Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys		
	210	215 220
Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly		
	225	230 235 240
Val Val Gln Asn Asn Arg Leu Arg Lys Tyr Ala Phe Glu Leu Lys Met		
	245	250 255
Asn Asp Leu Thr Tyr Phe Val Leu Ala Ala Glu Thr Glu Ser Asp Met		
	260	265 270
Asp Glu Trp Ile His Thr Leu Asn Arg Ile Leu Gln Ile Ser Pro Glu		
	275	280 285
Gly Pro Leu Gln Gly Arg Arg Ser Thr Glu Leu Thr Asp Leu Gly Leu		
	290	295 300
Asp Ser Leu Asp Asn Ser Val Thr Cys Glu Cys Thr Pro Glu Glu Thr		
	305	310 315 320
Asp Ser Ser Glu Asn Asn Leu His Ala Asp Phe Ala Lys Tyr Leu Thr		
	325	330 335
Glu Thr Glu Asp Thr Val Lys Thr Thr Arg Asn Met Glu Arg Leu Asn		
	340	345 350
Leu Phe Ser Leu Asp Pro Asp Ile Asp Thr Leu Lys Leu Gln Lys Lys		
	355	360 365
Asp Leu Leu Glu Pro Glu Ser Val Ile Lys Pro Phe Glu Glu Lys Ala		
	370	375 380
Ala Lys Arg Ile Met Ile Ile Cys Lys Ala Leu Asn Ser Asn Leu Gln		
	385	390 395 400
Gly Cys Val Thr Glu Asn Glu Asn Asp Pro Ile Thr Asn Ile Glu Pro		
	405	410 415
Phe Phe Val Ser Val Ala Leu Tyr Asp Leu Arg Asp Ser Arg Lys Ile		
	420	425 430
Ser Ala Asp Phe His Val Asp Leu Asn His Ala Ala Val Arg Gln Met		
	435	440 445
Leu Leu Gly Ala Ser Val Ala Leu Glu Asn Gly Asn Ile Asp Thr Ile		
	450	455 460

Thr Pro Arg Gln Ser Glu Glu Pro His Ile Lys Gly Leu Pro Glu Glu
 465 470 475 480
 Trp Leu Lys Phe Pro Lys Gln Ala Val Phe Ser Val Ser Asn Pro His
 485 490 495
 Ser Glu Ile Val Leu Val Ala Lys Ile Glu Lys Val Leu Met Gly Asn
 500 505 510
 Ile Ala Ser Gly Ala Glu Pro Tyr Ile Lys Asn Pro Asp Ser Asn Lys
 515 520 525
 Tyr Ala Gln Lys Ile Leu Lys Ser Asn Arg Gln Phe Cys Ser Lys Leu
 530 535 540
 Gly Lys Tyr Arg Arg Ala Phe Ala Trp Ala Val Arg Ser Val Phe Lys
 545 550 555 560
 Asp Asn Gln Gly Asn Val Asp Arg Asp Ser Arg Phe Ser Pro Leu Phe
 565 570 575
 Arg Gln Glu Ser Ser Lys Ile Ser Thr Glu Asp Leu Val Lys Leu Val
 580 585 590
 Ser Asp Tyr Arg Arg Ala Asp Arg Ile Ser Lys Met Gln Thr Ile Pro
 595 600 605
 Gly Ser Leu Asp Ile Ala Val Asp Asn Val Pro Leu Glu His Pro Asn
 610 615 620
 Cys Val Thr Ser Ser Phe Ile Pro Val Lys Pro Phe Asn Met Met Ala
 625 630 635 640
 Gln Thr Glu Pro Thr Val Glu Val Glu Glu Phe Val Tyr Asp Ser Thr
 645 650 655
 Lys Tyr Cys Arg Pro Tyr Arg Val Tyr Lys Asn Gln Ile Tyr Ile Tyr
 660 665 670
 Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg
 675 680 685
 Asn Ile Thr Val Cys Ile Glu Phe Lys Asn Ser Asp Glu Glu Ser Ala
 690 695 700
 Lys Pro Leu Lys Cys Ile Tyr Gly Lys Pro Glu Gly Pro Leu Phe Thr
 705 710 715 720
 Ser Ala Ala Tyr Thr Ala Val Leu His His Ser Gln Asn Pro Asp Phe
 725 730 735
 Ser Asp Glu Val Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His
 740 745 750
 His Ile Leu Phe Ser Phe Tyr His Val Thr Cys Asp Ile Asn Ala Lys
 755 760 765
 Ala Asn Ala Lys Lys Lys Glu Ala Leu Glu Thr Ser Val Gly Tyr Ala
 770 775 780

Trp Leu Pro Leu Met Lys His Asp Gln Ile Ala Ser Gln Glu Tyr Asn
 785 790 795 800
 Ile Pro Ile Ala Thr Ser Leu Pro Pro Asn Tyr Leu Ser Phe Gln Asp
 805 810 815
 Ser Ala Ser Gly Lys His Gly Gly Ser Asp Ile Lys Trp Val Asp Gly
 820 825 830
 Gly Lys Pro Leu Phe Lys Val Ser Thr Phe Val Val Ser Thr Val Asn
 835 840 845
 Thr Gln Asp Pro His Val Asn Ala Phe Phe Gln Glu Cys Gln Lys Arg
 850 855 860
 Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys
 865 870 875 880
 Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu
 885 890 895
 Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu
 900 905 910
 Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala
 915 920 925
 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
 930 935 940
 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
 945 950 955 960
 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
 965 970 975
 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
 980 985 990
 Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
 995 1000 1005
 Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
 1010 1015 1020
 Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr Lys Asp Ala Leu
 1025 1030 1035 1040
 Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg Phe Leu Lys Arg
 1045 1050 1055
 Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn
 1060 1065 1070
 Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr
 1075 1080 1085
 Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro
 1090 1095 1100
 Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro

1105	1110	1115	1120
Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser			
1125	1130	1135	
Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu			
1140	1145	1150	
Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu			
1155	1160	1165	
Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp			
1170	1175	1180	
Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met			
1185	1190	1195	1200
Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys			
1205	1210	1215	
Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp			
1220	1225	1230	
Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His			
1235	1240	1245	
Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile			
1250	1255	1260	
Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser			
1265	1270	1275	1280
Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys			
1285	1290	1295	
Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala			
1300	1305	1310	
Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr			
1315	1320	1325	
Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr			
1330	1335	1340	
Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser			
1345	1350	1355	1360
Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn Phe Arg Tyr Leu			
1365	1370	1375	
Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val			
1380	1385	1390	
Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys			
1395	1400	1405	
Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His			
1410	1415	1420	
Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly			
1425	1430	1435	1440

Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr
 1445 1450 1455
 Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr
 1460 1465 1470
 Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val
 1475 1480 1485
 Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys
 1490 1495 1500
 Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe
 1505 1510 1515 1520
 Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu
 1525 1530 1535
 Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala
 1540 1545 1550
 Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His
 1555 1560 1565
 Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe
 1570 1575 1580
 Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser
 1585 1590 1595 1600
 His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly
 1605 1610 1615
 Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe
 1620 1625 1630
 Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val
 1635 1640 1645
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1650 1655 1660
 Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1665 1670 1675 1680
 Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp
 1685 1690 1695
 Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
 1700 1705 1710
 Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
 1715 1720 1725
 Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
 1730 1735 1740
 Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
 1745 1750 1755 1760

Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
 1765 1770 1775
 Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
 1780 1785 1790
 Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
 1795 1800 1805
 Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
 1810 1815 1820
 Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
 1825 1830 1835 1840
 Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
 1845 1850 1855
 Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
 1860 1865 1870
 Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys
 1875 1880 1885
 Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
 1890 1895 1900
 Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
 1905 1910 1915 1920
 Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
 1925 1930 1935
 Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
 1940 1945 1950
 Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
 1955 1960 1965
 Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
 1970 1975 1980
 Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
 1985 1990 1995 2000
 His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser
 2005 2010 2015
 Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
 2020 2025 2030
 Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
 2035 2040 2045
 Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
 2050 2055 2060
 Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
 2065 2070 2075 2080
 Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg

2085	2090	2095
Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu 2100	2105	2110
Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr 2115	2120	2125
Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr 2130	2135	2140
Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg 2145	2150	2155 2160
Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val Ser Ile Ser Ser 2165	2170	2175
Ser Ala Glu Val 2180		

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 <213> Artificial Sequence

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31

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31

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34

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19

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21

B1
Cont

